Zeman, R. 09/284787 Seg.1051-3 4 Inters	9 1 PCT-US95-01467-14 Sequence 9 1 PCT-US97-15500-12 Sequence 9 1 PCT-US97-2034-11 Sequence 9 1 PCT-US98-06791-1 Sequence 9 1 PCT-US98-06791-1 Sequence 9 1 PCT-US98-01189-28 Sequence 9 1 PCT-US99-01189-28 Sequence 9 1 PCT-US99-01188-1 Sequence 9 1 PCT-US99-01488-1 Sequence 9 1 PCT-US99-01488-1 Sequence 9 1 PCT-US99-01488-2 Sequence 9 1 PCT-US99-01488-2 Sequence	100.0 9 4 US-08-017-9314-18 Sequence 19, Appl 100.0 9 4 US-08-092-977-19 Sequence 19, Appl 100.0 9 4 US-08-093-499-19 Sequence 19, Appl 100.0 9 5 US-08-108-191 Sequence 19, Appl 100.0 9 5 US-08-192-477-14 Sequence 19, Appl 100.0 9 5 US-08-196-043-19 Sequence 19, Appl 100.0 9 6 US-08-287-537-3 Sequence 19, Appl 100.0 9 6 US-08-295-595-19 Sequence 19, Appl 100.0 9 6 US-08-295-596-19 Sequence 19, Appl 100.0 9 6 US-08-295-596-19 Sequence 19, Appl 100.0 9 6 US-08-295-596-19 Sequence 19, Appl 100.0 9 8 US-08-43-982A-7 Sequence 3, Appl 100.0 9 8 US-08-45-753-3 Sequence 3, Appl 100.0 9 8 US-08-45-728-28 Sequence 28, Appl 100.0 9 8 US-08-465-772A-28 Sequence 28, Appl 100.0 9 8 US-08-465-772A-28 Sequence 28, Appl 100.0	sadnence sednence sednence sednence sednence sednence sednence sednence sednence sednence sednence sednence sednence	RESULT 1  FCT-US00-0507-17  Sequence 17, Application PC/TUS0005097  Sequence 17, Application PC/TUS0005097  GENERAL INFORMATION:  TITLE OF INVENTION: NOVEL TRANSDUCTION MOLECULES AND METHODS  TITLE OF INVENTION: NOVEL TRANSDUCTION MOLECULES AND METHODS  TITLE OF INVENTION: PCT USING SAME  FILE REFERENCE: 49054-PCT  CURRENT APPLICATION NUMBER: PCT/US00/05097  CURRENT FILING DATE: 1999-02-28  PRIOR PAPLICATION NUMBER: 60/122,757  PRIOR APPLICATION NUMBER: 60/151,291	LING DAIL: 1999-0-29 F SEQ ID NOS: 59-0-29 17 17 9 9 HT M: Unknown N: NFORMATION: Synthetic sequence	cch 100.0%; Score 55; DB 1; Length 9; 11 Similarity 100.0%; Pred. No. 2.9e+06; 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; PYDVPDXA 9
us-09-284-787-1.rapm	10 5 11 5 5 11 13 5 5 11 14 5 5 11 15 5 5 11 15 5 5 5 11 17 5 5 5 11 17 5 5 5 5	20 20 22 23 23 24 25 25 26 25 27 27 28 29 30 33 33 55 33 55	34 33 34 35 37 38 38 38 38 38 38 38 38 38 38 38 38 38	RESULT 1 PCT-US00-05097- ; Sequence 17, ; GENERAL INFO ; APPLICANT: ; TITLE OF INFO ; FILE REFERENCE ; CURRENT APPL ; CURRENT APPL ; CURRENT APPL ; CURRENT APPL ; PRIOR APPLICATION ; PRIOR PRIOR PRICE ; PRIOR PILINO	d,  App1	Appl         Query Match           Appl         Best Local           Appl         Matches           Appl         Qy         1 YPX           Appl         Qy         1 YPX           Appl         Db         1 YPX
11 15:31:04 2002	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. protein search, using sw model April 11, 2002, 10:14:10 ; Search time 266.73 Seconds (without alignments) 9.369 Million cell updates/s	US-09-284-787-1 55 1 YPYDVPDYA 9 5: BLOSUM62 Gapop 10.0 , Gapext 0.5 3148936 seqs, 277657034 residues of hits satisfying chosen parameters: 3148936 99 length: 0	" _ 40 w 4 w 0 v 8	9: /cgn2_6/ptodata/2/paa/US085_COMB.pep:* 10: /cgn2_6/ptodata/2/paa/US085_COMB.pep:* 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep:* 12: /cgn2_6/ptodata/2/paa/US087_COMB.pep:* 13: /cgn2_6/ptodata/2/paa/US089_COMB.pep:* 14: /cgn2_6/ptodata/2/paa/US091_COMB.pep:* 15: /cgn2_6/ptodata/2/paa/US091_COMB.pep:* 16: /cgn2_6/ptodata/2/paa/US091_COMB.pep:* 17: /cgn2_6/ptodata/2/paa/US091_COMB.pep:* 19: /cgn2_6/ptodata/2/paa/US094_COMB.pep:* 20: /cgn2_6/ptodata/2/paa/US094_COMB.pep:* 21: /cgn2_6/ptodata/2/paa/US096_COMB.pep:* 22: /cgn2_6/ptodata/2/paa/US096_COMB.pep:* 23: /cgn2_6/ptodata/2/paa/US099_COMB.pep:* 24: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*	eater than or equal to the score of the result being prin erived by analysis of the total score distribution.  SUMMARIES  Query  Match Length DB ID  Description	55 100.0 9 1 PCT-US00-06950-9 Sequence 9, R 5 100.0 9 1 PCT-US00-19198-20 Sequence 20, S 5 100.0 9 1 PCT-US00-20131A-28 Sequence 20, S 5 100.0 9 1 PCT-US00-20131A-43 Sequence 24, S 5 100.0 9 1 PCT-US00-22456-1 Sequence 43, S 5 100.0 9 1 PCT-US00-23456-1 Sequence 1, R 5 100.0 9 1 PCT-US00-3038-5 Sequence 5, S 5 100.0 9 1 PCT-US00-30238-5 Sequence 5, R 5 100.0 9 1 PCT-US93-12643-6 Sequence 6, R 5 100.0 9 1 PCT-
Thu Apr	OM protein - Run on:	Title: Perfect score: Sequence: Scoring table: Searched: Total number of Minimum DB seq Maximum DB seq			Pred.	~~ <del>~</del> ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~

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CURRENT FILING DATE: 2000-07-24
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
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PCT-US00-20131A-43
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PCT-US00-22456-1
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                                                                Sequence 9, Application PC/TUS0006950
GENERAL INFORMATION:
SPECTAGENE OR PORTATION:
TITLE OF INVENTION: METHODS FOR DETECTION OF NUCLEIC ACID POLYMORPHISMS USING
TITLE OF INVENTION: PEPTIDE-LABELED OLIGONUCLEOTIDES AND ANTIBODY ARRAYS
TILE REFERENCE: 9408-042-228
CURRENT APPLICATION NUMBER: PCT/US00/06950
CURRENT PILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 9
LENGTH: 9
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| GENERAL INFORMATION:
| APPLICANT: James S. HUSTON et al.
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
| TITLE OF INVENTION: ACCOUNTLATION ASSOCIATED WITH NEUROLOGICAL DISORDERS;
| FILE REFERENCE: INR-004PC
| CURRENT APPLICATION NUMBER: PCT/US00/20131A
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PCT-US00-19198-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Human Genome Sciences, Inc.
TILE DE INVENTION: Follstatin-3
FILE REFERENCE: PF38BPCT-2
CURRENT FILID END FOLSTON NUMBER: PCT/USOO/19198
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/144,088
PRIOR FILING DATE: 1999-07-16
NUMBER OF SEQ 1D NOS: 22
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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PCT-USO0-19198-20
; Sequence 20, Application PC/TUSO019198
; GENERAL INFORMATION Former Sciences, In-
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                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
9; Conserve
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ORGANISM: Primer_Bind
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-US00-06950-9
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
FILE REFERENCE: INR-004PC
CURRENT APPLICATION NUMBER: PCT/US00/20131A
CURRENT FILING DATE: 2000-07-27
PRIOR FILING DATE: 1999-07-27
RUMBER OF SEQ ID NOS: 45
SOFTWARE: PALCATION VET. 2.0
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: construct
PCT-USO0-20131A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: construct
PCT-US00-20131A-43
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GENERAL INFORMATION:
APPLICANT: Donald J. Buchsbaum
APPLICANT: Buck E. Rogers
APPLICANT: Gene Transfer Imaging and Uses Thereof
FILE REFERENCE: D5036CIPPCT
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: 09/374,972
PRIOR APPLICATION NUMBER: 09/374,972
PRIOR APPLICATION NUMBER: 09/374,972
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 55; DB 1; Length 9; 100.0%; Pred. No. 2.9e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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APPLICANT: James S. HUSTON et al.
PRIOR APPLICATION NUMBER: 60/146,047
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 9
                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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0; Gaps

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Length 9;
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APPLICANT: Lok, Si
TILLE OF INVENTION: Cell Surface Display of Proteins by
TITLE OF INVENTION: Recombinant Host Cells
FILE REFERENCE: 99-34
CURRENT APPLICATION NUMBER: PCT/USOO/30238
CURRENT FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 5
SSFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Roger Brent
APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND
TITLE OF INVENTION: RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB 1; 1
Pred. No. 2.9e+06;
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100.0%; Pred. No. 2.9e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Hemagglutinin A epitope tag
PCT-USO0-30238-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 02110-2804
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12643
FILING DATE: 29-DEC-1993
CLASSIFICATION:
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ARR: 00786/160001
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APPLICATION NUMBER: 08/011,398
FILLING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/1º
TELECOMMUNICATION INFORMATION:
TELECHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application PC/TUS9312643 GENERAL INFORMATION:
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100.0%;
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ORGANISM: Artificial Sequence
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
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STRANDEDNESS: N/
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TOPOLOGY:
PCT-US93-12643-6
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PCT-US93-12643-6
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cunningham, Sonia
Barros, Maria Pia
TITLE OF INVENTION: A POLYNUCLEOTIDE ENCODING A HUMAN
JUNCTIONAL ADHESION PROTEIN (JAM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
Sulte 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
FILING DATE: 23-049-2000
CLASSIFCATION: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 55; DB 1; Length 9; 100.0%; Pred. No. 2.9e+06; Live 0; Mismatches 0; Indels
                                                                                                                                                                     100.0%; Score 55; DB 1; Length 9; 100.0%; Pred. No. 2.9e+06;
                                                                                                                                                                                                              Indels
                                                            FEATURE:
; OTHER INFORMATION: amino acid sequence of "HA" tag
PCT-US00-22456-1
                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 25,011 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
PCT-US00-30238-5
PCT-US00-30238-5
Sequence 5, Application PC/TUS0030238
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 312-616-5400
TELERAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Katz, Martin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                            TYPE: PRT
ORGANISM: Artificial sequence
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                                                                                                                                               Query Match
Best Local Similarity 100...
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
                                                                                                                                                                                                                                                                           1 YPYDVPDYA 9
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PCT-US00-23158-10
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APPLICANT:
TITLE OF INVENTION: COMPOSITIONS AND USES FOR A NOVEL CELL
TITLE OF INVENTION: DEATH PROTECTING PROTEIN
NUMBER OF SEQUENCES: 12
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/15500 FILING DATE: 03-SEP-1997 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 55; DB 1; 100.0%; Pred. No. 2.9e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/030,302
FILING DATE: 05-NOV-1996
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
PCT-US97-20344-11
; Sequence 11, Application PC/TUS9720344
; GENERAL INFORMATION:
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025,370
FILING DATE: 03-SEP-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US UNKNOWN
FILLING DATE: 04-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,:
                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0847;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows
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                                   ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR EQG ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids:
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Best Local Similarity 100.

Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein PCT-US97-15500-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
PCT-US97-20344-11
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                      COUNTRY:
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GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO
TITLE OF INVENTION: OVERPRODUCE PEPTIDES AND PROTEINS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 9;
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TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01467
FILING DATE: 03-FEB-1995
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1880 Century Park East, Suite 500
  Mismatches
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100.0%; Pred. No. 2.9
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: BOSTICH, June M.
REGISTRATION NUMBER: 31,238
REFERENCE/DOCKET NUMBER: FD-4(
TELECOMMUNICATION INFORMATION:
TELEFRAN: (619) 455-5100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acids
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Best Local Similarity 100.

Matches 9; Conservative
9; Conservative
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CLONE: 12CA5
                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Peptide LOCATION: 1..9
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                                     1 YPYDVPDYA 9
                                                            1 YPYDVPDYA 9
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                      9006
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                                                                                                                                                          PCT-US95-01467-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
CITY: BC
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  Matches
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Length 9; Indels us-09-284-787-1.rapm

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APPLICANT: Hall, Frederick L.
APPLICANT: Hall, Frederick L.
APPLICANT: Hall, Erederick L.
APPLICANT: Hall, Edwin Lingtao
APPLICANT: Hall, Bone Morphogenetic
TITLE OF INVENTION: Bone Morphogenetic
TITLE OF INVENTION: Proteins and Their Use in Bone Growth
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABCCHARALT & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 55; DB 1; I
100.0%; Pred. No. 2.9e+06;
/ative 0; Mismatches 0;
                                                                                                    NAME: CROOK, WANNELL M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 3595-2-PCT
TELECOMINICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-023
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 9002-335
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/11189
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US98-11189-28; Sequence 28, Application PC/TUS9811189; GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/868,452
FILING DATE: 3-June-1997
ATTORNEY/AGENT INFORMATION:
NAME: WOOG, William J.
REGISTRATION NUMBER: P-42,236
REFRENCE/DOCKET NUMBER: 30853-11
TELECOMMUNICATION INFORMATION:
                                                           FILING DATE: 03-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 310-445-1141
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein PCT-US98-06791-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: INACTIVATION OF HIV CO-RECEPTORS AS THERAPY TITLE OF INVENTION: FOR HIV INFECTION NUMBER OF SEQUENCES: 6
                                             Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 55; DB 1; Length 9; 100.0%; Pred. No. 2.9e+06;
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GENERAL INFORMATION:
APPLICANT: PORT, J D.
APPLICANT: BRISTOW, MICHAEL R.
TITLE OF INVENTION: "TRANSCENIC MODEL AND TREATMENT FOR TITLE OF INVENTION: HEART DISEASE"
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/22198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                      100.0%; Score 55; DB 1; 1
100.0%; Pred. No. 2.9e+06;
ive 0; Mismatches 0;
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FILING DATE:
CLASSIFICATION:
PRIOR PAPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DOI:
1. NFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
1. LENGTH: 9 amino acids
TYPE: amino acids
TYPE: amino acids
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STREET: 1700 LINCOLN ST., SUITE 3500
CITY: DENVER
STATE: COLORADO
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/06791
FILING DATE:
                                                                                                                                                                                                                                                                            Sequence 1, Application PC/TUS9722198
GENERAL INFORMATION:
APPLICANT:
                                    Query Match
Best Local Similarity 100.
Matches 9: Conservative
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Matches 9; Conservative
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PCT-US97-22198-1
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PCT-US97-22198-1
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; MOLECULE TYPE: protein PCT-US98-11189-28
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0; Gaps Query Match 100.0%; Score 55; DB 1; Length 9; Best Local Similarity 100.0%; Pred. No. 2.9e+06; Matches 9; Conservative 0; Mismatches 0; Indels οy

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Search completed: April 11, 2002, 10:20:50 Job time: 400 sec

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TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
GENES AND OTHER BIOLOGICAL EVENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT TO CAGE
APPLICANT THE GENERAL HOSPITAI CORPORATION
APPLICANT Scadden, David T.
APPLICANT Lee, Byeong-Chel
TITLE OF INVENTION: METHODS AND PRODUCTS FOR MANIPULATING
TITLE OF INVENTION: METHODS AND PRODUCTS FOR MANIPULATING
TITLE OF INVENTION: METHODS AND PRODUCTS FOR CELES
FILE REPRENCE: M0765,7039W0,768C/AS
CURRENT APLICATION NUMBER: PCT/US01/45076
CURRENT FILING DATE: 2001-11-29
RIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 10
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100.0%; Pred. No. 3.1e+05;
US-09-352-171-7
US-09-620-9558-28
US-09-620-9558-43
US-10-001-073-23
US-10-001-073-23
US-10-003-178-10
US-10-003-178-10
US-10-003-178-10
US-10-003-178-10
US-10-003-178-10
US-10-003-178-10
US-10-003-178-10
US-09-563-055-1
US-09-563-055-1
US-09-656-466-25
US-09-665-466-25
US-09-665-466-25
US-09-615-40
US-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Spencer, David M.
Wandless, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-09-466-568-19
Sequence 19, Application US/09466568
GENERAL INFORMATION:
APPLICANT: Crabtree, Gerald R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 9, Application PC/TUS0145076
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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PCT-US01-45076-9
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Best Local Similarity
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     1 YPYDVPDYA
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PCT-US01-45076-9
        TYPE: PRT
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Sequence 17,
Sequence 32,
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USOG_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USOR_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*
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                                                             Compugen Ltd
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US-09-931-381A-24

US-09-180-167A-17

US-09-775-052A-17

US-09-574-733-32

US-09-574-733-32

US-09-574-733-32

US-09-574-733-32

US-09-574-733-32

US-09-985-874-4

US-09-95-874-4

US-09-95-874-4

US-09-574-73-8858-7

US-09-713-8858-7

US-09-713-8858-7

US-09-714-471-7

US-09-714-471-7

US-09-830-985-847-4

US-09-714-471-7

US-09-714-471-7

US-09-830-985-847-4
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                                   version 4.5
- 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                GenCore
Copyright (c) 1993
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length: 2000000000
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Maximum DB seq
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Sequence 9, Application US/09936969

SEQUENCE INFORMATION:
APPLICANT: INFORMATION:
APPLICANT: INFORMATION:
APPLICANT: POULNY, J.
APPLICANT: POULNY, J.
TITLE OF INVENTION: PEFFIDE-LABELED OLIGONUCLEOTIDES AND ANTIBODY ARRAYS
FILE REFERENCE: 9408-042-999
CURRENT APPLICATION NUMBER: US/09/936,969
CURRENT FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 9
LENGTH: 9
                           Gaps
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                         Indels
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100.0%; Pred. No. 3.1e+05; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 55; DB 5; I
100.0%; Pred. No. 3.1e+05;
tive 0; Mismatches 0;
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llarity 100.0%; Pred. No. 3.1e+05;
Conservative 0; Mismatches 0;
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; OTHER INFORMATION: Oryctolagus cuniculus
US-09-936-969-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-180-167A-17; Sequence 17, Application US/09180167A; Sequence 17, Application US/09180167A; APPLICANT: Gordon C. Shore et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                         9; Conservative
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Best Local Similarity
Matches 9; Conserv
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Matches 9; Conserv
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Sequence 24, Application US/09931381A

GENERAL INCOMMATION:
APPLICANT: Butcher, Eugene C.
APPLICANT: Runkel, Erc J.
APPLICANT: Runkel, Erc J.
APPLICANT: Pan, Junliang
APPLICANT: Soler-Ferran, Dulce
TITLE OF INVENTION: Method for Identifying Agents Which
TITLE OF INVENTION: Modulate Chemokine "MEC"-Induced Functions of CCR3 and/or
TITLE OF INVENTION: Modulate Chemokine "MEC"-Induced Functions of CCR3 and/or
TITLE OF INVENTION: CCR10
TITLE OF INVENTION: MODIBER: US/09/931,381A
TITLE OF INVENTION NUMBER: US/09/931,381A
CURRENT FILING DATE: 2000-08-15
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 24
LENGTH: 9
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                                                                                  COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC/DOS/MS/DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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100.0%; Pred. No. 3.1e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Figg, E. Anthony
REGISTRATION NUMBER: 27,195
REFERENCE/DOCKET NUMBER: 2054-114A
TELEFORMICATION INFORMATION:
TELEFORM: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/157,753
FILING DATE: «UNKNOWN)
APPLICATION NUMBER: 08/388,653
FILING DATE: 14 FEB-1995
APPLICATION NUMBER: US 08/478,386
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/466,568
FILING DATE: 17-Dec-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 19: US-09-466-568-19
STREET: 26 Landsdowne Street
                    CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
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Best Local Similarity 100.
Matches 9; Conservative
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DB 5;

100.0%; Score 55;

Query Match

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GENERAL INFORMATION:
APPLICANT: Wang, Zhou
APPLICANT: Xiao, Wuhan
APPLICANT: Xiao, Wuhan
APPLICANT: NATHOLO OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
FILE REFERENCE: 1720-1-001CIP
CURRENT APPLICATION NUMBER: US/09/906,393A
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/218,761
PRIOR FILING DATE: 2000-07-17
APPLICANT: Krols, Luc
TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
FILE REFERENCE: 2283/310
CURRENT APPLICATION NUMBER: US/09/574,735C
CURRENT APPLICATION NUMBER: US/09/574,735C
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.0
SEQ ID NO 45
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                       Length 9;
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APPLICANT: Sharp, Phillip A.
APPLICANT: Pado, Carl O.
TITLE OF INVENTION: Chimeric DNA-binding proteins
FILE REFERENCE: APV-022.02
CURRENT APPLICATION NUMBER: 08/09/652,370A
CURRENT FILING DATE: 1001-05-10
PRIOR APPLICATION NUMBER: 08/973,131
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: PCT/US95/16982
PRIOR FILING DATE: 1995-12-29
PRIOR FILING DATE: 1994-12-29
PRIOR FILING DATE: 1994-12-29
                                                                                                                                                                                                                                                                                                                       100.0%; Score 55; DB 6; I 100.0%; Pred. No. 3.1e+05;
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100.0%; Pred. No. 3.1e+05;
iive 0; Mismatches 0;
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Best Local Similarity 100.vv
Pest a 9; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 33
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                    Conservative
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US-09-574-735C-45
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
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GENERAL INFORMATION:
APPLICANT: Ward, Michael
APPLICANT: Ward, Michael
APPLICANT: Ward, Michael
APPLICANT: Ward, Michael
APPLICANT: Power, Scott D.
TITLE OF INVENTION: DNA SEQUENCES, VECTORS, AND FUSION POLYPEPTIDES FOR SECRETION OF TITLE OF INVENTION: POLYPEPTIDES IN FILAMENTOUS FUNGI
FILE REPERBNCE: A-62926-1
CURRENT APPLICATION NUMBER: US/09/912,733
CURRENT FILING DATE: 2001-07-23
PRIOR PILING DATE: 1997-01-17
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 32
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                                                                                                       APPLICANT DOWGY, Steven F.

TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF FILE REFERENCE: 48881/1742
CURRENT APPLICATION NUMBER: US/09/775,052A
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/069,012
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PATENTING VOT: 2.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULY
US-09-574-735C-45
Sequence 45, Application US/09574735C
SEREMAL INFORMATION:
APPLICANT: Beeckman, Tom
APPLICANT: Inz,, Dirk
APPLICANT: Van Camp, Wim
                                                                    Sequence 17, Application US/09775052A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic. US-09-912-733-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 9
TYPE: PRT
ORGANISM: human
US-09-775-052A-17
                                            US-09-775-052A-17
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Alessi, Dario
Cross, Darren
TITLE OF INVENTION: CONTEN SYNTHESIS, AND SCREENING METHOD
FOR AGENTS
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                                                                                                                                                                       Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 55; DB 6; 1
100.0%; Pred. No. 3.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/091,763
FILING DATE: 19-JUN-1998
APPLICATION NUMBER: PCT/GB96/03186
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: GB 9526083.2
FILING DATE: 20-DEC-1995
APPLICATION NUMBER: GB 9610272.8
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: GB 9615066.9
FILING DATE: 18-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
RADRESSEE: Braman & Rogalskyj, LLP
STREET: P.O. Box 352
CIT: Canandalgua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 32: US-09-845-667-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/09845667
GENERAL INFORMATION:
APPLICANT: Cohen, Philip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 716-393-3002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
SEQ ID NO 53
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                             ; OTHER INFORMATION: Peptide US-09-554-726A-53
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 14424-0352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
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Sequence 53, Application US/09554726A

GENERAL INFORMATION:

APPLICANT: HERRANN, Bernhard

APPLICANT: KISPERT, Andreas

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 258,0009 0101

CURRENT APPLICATION NUMBER: US/09/554,726A

CURRENT APPLICATION NUMBER: PG7/FP 98/07395

PRIOR APPLICATION NUMBER: EP 98/07395

PRIOR APPLICATION NUMBER: EP 98 10 3596.7

PRIOR FILING DATE: 1998-03-02

PRIOR FILING DATE: 1998-03-02

PRIOR PLING DATE: 1998-11-18

PRIOR FILING DATE: 1998-11-18

PRIOR FILING DATE: 1998-03-02

PRIOR FILING DATE: 1998-03-02

PRIOR FILING DATE: 1998-03-02

WINNER OF SEQ ID NOS: 53

SOFTWARE: PATENTIN VETSION 3.1
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GENERAL INFORMATION:
APPLICANT: Dowdy, Steven F.
TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF FILE REFERENCE: 4881/1742
CURRENT APPLICATION NUMBER: US/09/775,052
CURRENT FILING DATE: 2001-02-01
PRIOR FILING DATE: 1998-12-10
PRIOR FILING DATE: 1999-12-10
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0; Mismatches 0;
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Pred. No. 3
                                                                                                                                                                                                          100.0%;
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100.0%;
                 SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 9
                                                                                         ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                              ; OTHER INFORMATION: HA Tag
US-09-906-393A-4
 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                     1 YPYDVPDYA 9
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US-09-775-052-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-554-726A-53
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                                                                         TYPE: PRT
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Gaps

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                                                                       100.0%; Score 55; DB 6; Length 9; 100.0%; Pred. No. 3.1e+05; ive 0; Mismatches 0; Indels
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                                                                       Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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       US-09-554-726A-53
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US-09-554-726A-53
Sequence 53, Application US/09554726A
Sequence 53, Application US/09554726A
Sequence 53, Application US/09554726A
Sequence 54, Application US/09554726A
Sevence 55, Application US/09554726A
APPLICANT: KISPERT, Andreas
TITLE OF INVENTION: UNCLEIC ACIDS INVOLVED IN THE RESPONDER PHENOTYPE AND APPLICATION
TITLE OF INVENTION: THEREOF
FILE REPERENCE: 258 0009 0101
CURRENT APPLICATION NUMBER: US/09/554,726A
CURRENT FILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-00-02
PRIOR APPLICATION NUMBER: EP 97 12 0190.0
PRIOR FILING DATE: 1997-11-18
SEQ ID NOS: 53
SOFTWARE: PAGENTIAL OF SEQ ID NOS: 53
LENGTH: 9
LENGTH: 9
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APPLICANT: Church, George
APPLICANT: Church, George
APPLICANT: Church, George
APPLICANT: Church, George
APPLICANT: Church, Bin
APPLICANT: Schwartz, John
APPLICANT: Lugovskoy, Alaxey
TITLE OF INVENTION: MODULAR MOLECULAR CLASPS AND USES THEREOF
TITLE OF INVENTION: MODULAR MOLECULAR CLASPS AND USES THEREOF
TITLE OF INVENTION: MOMBER: US/09/995,847
CURRENT APPLICATION NUMBER: 60/279,524
PRIOR FILING DATE: 2001-01-28
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 20
SEQTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: HA epitope US-09-995-847-4
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  100.0%; Score 55; DB 6; Length 9; 100.0%; Pred. No. 3.1e+05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                  Sequence 4, Application US/09995847
GENERAL INFORMATION:
APPLICANT: Rizzuto, Carlo
APPLICANT: AFEYAN, Noubar
APPLICANT: Lee, Frank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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Title: Perfect score:

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protein

Run on:

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DB DB

Minimum Maximum Database

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APPLICANT: Roche Diagnostics GmbH
TITLE OF INVENTION: Monoclonal Antibodies Against the Epitope YPYDVPDYA, A Process
TITLE OF INVENTION: Producing the Same and their Use
TITLE OF INVENTION: PRODUCING THE SAME AND THE SAME APPLICATION NUMBER: US/09/284,787
CURRENT APPLICATION NUMBER: PCT/EP97/05783
PRIOR FILING DATE: 1997-10-20
PRIOR FILING DATE: 1997-10-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VERSION 3.0
                              Sequence 15, Appl Sequence 15, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 64, Appl Sequence 2, Appl Sequence 13, Appl Sequence 13, Appl Sequence 169, Appl Sequence 16, Appl Sequence 17, Appl Sequence 18, Appl Sequence 2, Appl Sequence 3, Appl Sequence 4, Appl Sequence 6, 
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                              US-09-459-113A-15

US-09-7459-113A-15

US-08-787-738B-51

US-08-787-738B-51

US-08-787-738B-51

US-08-787-738B-51

US-08-963-368-51

US-08-963-368-8

US-08-911-2

US-09-215-2

US-09-211-2

US-09-211-127

US-09-954-043-13

US-09-954-043-13

US-09-954-043-13

US-09-954-043-13

US-09-954-043-13

US-09-951-144-8

US-08-592-007-169

US-08-592-007-169

US-08-592-007-169

US-08-592-007-169

US-08-592-1144-8

US-09-921-144-16

US-09-921-144-16

US-09-921-144-16

US-09-921-144-16

US-09-921-144-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: human influenza virus
US-09-284-787-2
1 YPYDVPDYAGSGSK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YPYDVPDYAGSGSK 14
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US-09-780-224A-11
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  SEQ ID NO 2
qq
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Sequence 7, Appli
Sequence 7, Appli
                                                                                                                          April 11, 2002, 10:20:50 ; Search time 266.73 Seconds (without alignments) 14.574 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, t
Sequence 11,
Sequence 56,
Sequence 23,
Sequence 22,
Sequence 22,
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/cgn2_6/ptodata/2/paa/US60_COMB.pep:*
                  4.5
Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-284-787-2
US-09-780-224A-11
US-09-475-158-56
US-09-622-646-23
US-09-622-646-25
PCT-US00-09002-11
PCT-US98-16887-7
US-09-134-793-7
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                  GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 YPYDVPDYAGSGSK 14
                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
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Match Length
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75
67
67
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65
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169, App 6, Appl1 8, Appl1

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Gaps

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Result Š

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Sequence 25, Application US/09622646
GENERAL INFORMATION:
APPLICANT: OZAKI, YASUKO
APPLICANT: CASHIHARA, YASUKO
TITLE OF INVENTION: IMMUNOCHEMICAL ASSAY FOR ANTI-HM1.24 ANTIBODY
FILE REFERENCE: 053466/0286
CURRENT APPLICATION NUMBER: US/09/622,646
      CURRENT APPLICATION NUMBER: US/09/622,646
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/JP99/00885
PRIOR FILING DATE: 1999-02-25
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                          83.8%;
78.6%;
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Best Local Similarity 78.6
Matches 11; Conservative
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US-09-622-646-22
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                                                                                                                                                                                                                                TYPE: PRT
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; GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry M.
APPLICANT: Fotts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Thereof and Novel Tethered Ligand-Receptor Molecules
TITLE OF INVENTION: Thereof and Novel Tethered Ligand-Receptor Molecules
FILE REFERENCE: 0609, 478001
CURRENT APPLICATION NUMBER: US 60/14,577
FRICR RELIGING DATE: 1999-12-30
PRIOR FILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 56
LENGTH: 32
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Sequence 11, Application US/09780224A
GENERAL INFORMATION:
APPLICANT: Roelvihk, Petrus W
APPLICANT: Roelvihk, Petrus W
APPLICANT: Wickham, Thomas J
TITLE OF INVENTION: ADENOVIRAL CAPSID CONTAINING CHIMERIC PROTEIN IX
FILE REFERENCE: 208659
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,163
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 11
LENGTH: 165
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US-09-475-158-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NS-09-622-646-23
Sequence 23, Application US/09622646
GENERAL INFORMATION:
APPLICANT: OZANI, YASUKO
APPLICANT: KOISHIHARA, YASUKO
TITLE OF INVENTION: IMMUNOCHEMICAL ASSAY FOR ANTI-HM1.24 ANTIBODY
FILE REFERENCE: 053466/0286
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 165;
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100.0%; Pred. No. 0.00047;
iive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 13; Conservative
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ORGANISM: Adenovirus
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Best Local Similarity
Matches 11; Conserv
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US-09-475-158-56
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; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence; OTHER INFORMATION: of a fusion protein comprising HA peptide and; OTHER INFORMATION: C-terminal-lacking soluble HM 1.24 antigenic protein US-09-622-646-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of The Information of a fusion protein comprising HA peptide and soluble OCHER INFORMATION: HM 1.24 antigenic protein US-09-622-646-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22, Application US/09622646
GENERAL INFORMATION:
APPLICANT: OZAKI, YASUKO
APPLICANT: OZAKI, YASUKO
TITLE OF INVENTION: IMMUNOCHEMICAL ASSAY FOR ANTI-HM1.24 ANTIBODY
FILE REFERENCE: 053466/0286
CURRENT APPLICATION NUMBER: US/09/622,646
CURRENT FILING DATE: 1099-02-25
PRIOR APPLICATION NUMBER: PCT/JP99/00885
PRIOR APPLICATION NUMBER: JP 10-60613
PRIOR APPLICATION NUMBER: JP 10-60613
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 22
LENGTH: 143
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Pred. No. 0.0073;
2; Mismatches 1; Indels
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81.2%; Score 65; DB 1; Length 16;
100.0%; Pred. No. 0.0014;
Live 0; Mismatches 0; Indels
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APPLICANT: Jessee, Joel A.
TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
                                       COMPUTER: DISKette
COMPUTER: DISKette
COMPUTER: DISKette
COMPUTER: IBM COMPATIBLE
COMPUTER: TBM COMPATIBLE
COMPUTER: TBM COMPATIBLE
SETMANTING SYSTEM: DOS
SOFFWATING SYSTEM: DOS
SOFFWATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: FOT/US98/16887
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION
APPLICATION NUMBER: 60/056,713
FILING DATE: 22-AUG-1997
ATTORNEY-AGENT INPORMATION:
NAME: CORIESS, PREETE F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 47275-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastESQ for Windows Version 2.0
CURRENT APPLICATION DATE: US/09/134,793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/056,713
FILING DATE: 22-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09134793 GENERAL INFORMATION:
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REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
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Best Local Similarity 100.
Matches 11; Conservative
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
        ZIP: 02109
COMPUTER READABLE FORM:
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STATE: MA
COUNTRY: USA
TE: 02109
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US-09-622-646-25
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GENERAL INFORMATION:
APPLICAMY: Mayo Foundation for Medical Education and Research et al.
TITLE OF INVENTION: Anti-apoptotic fusion polypeptide
FILE REFERENCE: 150.195M01
CURRENT APPLICATION NUMBER: PCT/US00/09002
CURRENT FILING DATE: 2000-0670/128,021
EARLIER APPLICATION NUMBER: US 60/128,021
EARLIER APPLICATION NUMBER: US 60/128,021
EARLIER FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 0.0087;
2; Mismatches 1; Indels
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GENERAL INFORMATION:
APPLICANT: Washington University
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/JP99/00885
PRIOR FILING DATE: 1999-02-25
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 29
SEQ YEARARE: PALENTIN VEr. 2.1
LENGTH: 147
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Best Local Similarity 78.0.
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Best Local Similarity 100.
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-US00-09002-11
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PCT-US98-16887-7
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LENGTH: 16
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                                                                                                                                                                                                TYPE: PRT
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Length 16;

Score 65; DB 17; Pred. No. 0.0014;

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81.2%; 8
100.0%;
                             Query Match 81.2
Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserva
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ORGANISM: Unknown
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US-09-459-113A-15
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SEQ ID NO 15
LENGTH: 16
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DOMON:
TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM AND USE THEREOF
FILE REPERENCE: 1142/47275
CURRENT APPLICATION UNMER: US/09/134,793A
CURRENT FILING DATE: 1998-08-14
SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09300639B
GENERAL INFORMATION:
APPLICANT: Steven F. Dowdy
TITLE OF INVENTION: Methods for Transducing Fusion Molecules
FILE REFERENCE: 48031
CURRENT APPLICATION NUMBER: US/09/300,639B
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/083,380
PRIOR FILING DATE: 1998-04-28
                                                                                                                                                                                                                                   Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 16;
                                                                                                                                                                                                                                 81.2%; Score 65; DB 15; Length 16
100.0%; Pred. No. 0.0014;
ive 0; Mismatches 0; Indels
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Pred. No. 0.0014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.2%; SCC.
100.0%; Pre
0; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
.currHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX:
                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-134-793-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                      4 YPYDVPDYAGS 14
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-134-793A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 16
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GENERAL INFORMATION:
APPLICANT: DOMOY.
TITLE OF INVERTION NOVEL TRANSDUCTION MOLECULES AND METHODS FOR USING SAME FILE REFERENCE: 49054(71742)
FILE REFERENCE: 49054(71742)
CURRENT APPLICATION NUMBER: 0S/09/514,673
CURRENT PELING DATE: 2000-02-28
PRIOR PELICATION NUMBER: 60/122,757
PRIOR FILING DATE: 1999-08-29
RIOR FILING DATE: 1999-08-29
RIOR FILING DATE: 1999-08-29
NUMBER: OSFTWARRE: PATENTIN Ver. 2.1
SEQ. ID NO 15
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                                                                                                                                                                                                                    Sequence 15, Application US/09459113A
GENERAL INFORMATION:
APPLICANT: Steven F. Dowdy
TITLE OF INVENTION: PROTEIN TRANSDUCTION SYSTEM AND METHODS
TITLE OF INVENTION: OF USE THEREOF
FILE REFERENCE: 48,884 (1742)
CURRENT APPLICATION NUMBER: US/09/459,113A
CURRENT FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 60/111,701
PRIOR APPLICATION NUMBER: 60/111,701
PRIOR PILING DATE: 1999-12-10
NUMBER OF SED ID NOS: 56
SOFTWARE: FRASEQ FOR WINDOWS Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.2%; Score 65; DB 18; Length 16; 100.0%; Pred. No. 0.0014; ive 0; Mismatches 0; Indels
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ilarity 100.0%; Pred. No. 0.0014;
Conservative 0; Mismatches 0;
     Mismatches
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0;
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Best Local Similarity 100.
Matches 11; Conservative
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US-08-17-138B-51
Sequence 51, Application US/08787738B
GENERAL INFORMATION:
APPLICANT: Nolan, Garry P
APPLICANT: Nolan, Garry P
TILE OF INVENTION: PEPTIDES AND RNA MOLECULES
TILLE REFERENCE: A-64259-1 correction
TILLE OF INVENTION: PEPTIDES AND RNA MOLECULES
FILE REFERENCE: A-64259-1 correction
CURRENT APPLICATION NUMBER: US/08/787,738B
CURRENT FILING DATE: 2001-09-18
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
Sequence 51, Application US/0878738

GENERAL INFORMATION:
APPLICANT: Nolan, Garry P
APPLICANT: Nolan, Garry P
APPLICANT: Nolan METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
FILE REFERENCE: A-64259-1 correction
CURRENT APPLICATION NUMBER: 08/089/108
PRIOR PLILNG DATE: 1096-01-23
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
SPRIOR FILING DATE: 1996-01-23
SURVARER OF SEQ ID NOS: 97
SEGRETARE PATENTIN Ver. 2.0
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81.2%; Score 65; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 11; Conservative 0; Mismatches 0; Indels
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Search completed: April 11, 2002, 10:20:51 Job time: 401 sec

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                                  Sequence 15, Application US/09775052A
GENERAL INFORMATION:
FIGHER INFORMATION:
CURRENT: DOWGY, Steven F.
TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
FILE REFERENCE: 48891/1742
CURRENT APPLICATION NUMBER: US/09/775,052A
CURRENT FILING DATE: EARLIER FILING DATE: 1998-12-10
PRIOR APPLICATION NUMBER: EARLIER PEPLICATION NUMBER: 60/069,012
PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10
PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10
SOFTWARE: PALENTING VOC. 2.0
SEQ ID NO 15
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 Sequence Seq
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US-09-775-052A-17
US-09-514-733-32
US-09-652-370A-33
US-09-662-370A-33
US-09-90-175-052-17
US-09-775-052-17
US-09-554-726A-53
US-09-955-106A-16
US-09-95-106A-16
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US-09-98-317-7
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Pred. No. 3.7e-05
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GENERAL INFORMATION:
APPLICANT: Medical Research Council
APPLICANT: Grifiths, Andrew
TITLE OF INVENTION: Optical Sorting Method
FILE REFERENCE: 18996/2022
CURRENT APPLICATION NUMBER: US/09/896,915
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: GB9900298.2
PRIOR APPLICATION NUMBER: PCT/GB00/00030
PRIOR APPLICATION NUMBER: PCT/GB00/00030
PRIOR FILING DATE: 2000-01-06
NUMBER: OF SEQ ID NOS: 40
SCOTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 34
TYPE: PRT
TYPE: PRT
US-09-896-915-8
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92.3%;
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nes 12; Conservative
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   RESULT 2
US-09-775-052A-15
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   Query Match
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Matches
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  (without alignments)
26.171 Million cell updates/sec
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Sequence 15,
Sequence 51,
Sequence 51,
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Sequence 2
Sequence 1
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Sequence 3
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Sequence 2
Sequence 2
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2: /cgn2_6/ptodateA/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodateA/2/paa/USO8_NEW_COMB.pep:*

4: /cgn2_6/ptodateA/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodateA/2/paa/USO8_NEW_COMB.pep:*

6: /cgn2_6/ptodateA/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodateA/2/paa/USO8_NEW_COMB.pep:*

8: /cgn2_6/ptodateA/2/paa/USO8_NEW_COMB.pep:*

8: /cgn2_6/ptodateA/2/paa/USO8_NEW_COMB.pep:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-976-940-51
US-10-096-550-51
US-09-98-2088-2
US-09-740-876-1
US-09-740-876-1
US-09-626-581C-57
US-09-626-581C-57
US-09-626-581C-57
US-09-626-581C-57
US-09-626-581C-57
US-09-616-508-34
US-09-616-508-34
US-09-616-508-34
US-09-618-32
US-10-002-24-33
US-10-002-24-25
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US-10-002-24-25
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US-10-015-535-22
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US-10-015-535-22
US-10-015-535-23
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US-09-936-969-9
US-09-180-167A-17
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US-09-466-568-19
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB seq
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Perfect score:
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TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR

TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR

TITLE OF INVENTION: BEFRETOR BEPTIDES AND RNA MOLECULES

FILE REPRENCE: A -64260 - 67RMS_AMS

CURRENT APPLICATION NUMBER: US/09/916,940

CURRENT FILING DATE: 2000-11-28

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1996-01-23

PRIOR FILING DATE: 1996-01-23

PRIOR FILING DATE: 1996-01-23

PRIOR FILING DATE: 1997-01-23

SOFTWARE: PATCHT NOW UNMBER: US 08/789,738

NUMBER OF SEQ ID NOS: 102

SSOFTWARE: PATCHT NOW VET. 2.0
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GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Dowly, Steven F.
TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
TITLE OF INVENTION: ANDWER: 2001-02-01
CURRENT APPLICATION NUMBER: 09/208,966
FRIOR APPLICATION NUMBER: 09/208,966
FRIOR APPLICATION NUMBER: 60/082,402
FRIOR APPLICATION NUMBER: 60/082,402
FRIOR APPLICATION NUMBER: 60/082,402
FRIOR APPLICATION NUMBER: 60/082,402
FRIOR APPLICATION NUMBER: 60/069,012
FRIOR APPLICATION NUMBER: 60/069,012
FRIOR PILING DATE: 1999-04-20
FRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 57
SOFTWARE PATENTING DATE: 1905-12-10
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                                                                                                                                               Length 16;
                                                                                                                                                                                               0; Indels
                                                                                                                                               Score 65; DB 5; L
Pred. No. 0.00016;
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                                                                                                                                            81.2%; ;
100.0%;
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                       4 YPYDVPDYAGS 14
                                                                                                                                                                                                                                                1 YPYDVPDYAGS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YPYDVPDYAGS 11
                    ; TYPE: PRT
; ORGANISM: human
US-09-775-052A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: human
US-09-775-052-15
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US-09-775-052-15
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LENGTH: 16
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Sequence 2, Application US/09892208A

GENERAL INFORMATION:

APPLICANT: Goldman, Stanley
APPLICANT: Goldman, Stanley
APPLICANT: Lathrop, Stephanie J.
APPLICANT: Longchamp, Pascal F.
APPLICANT: Longchamp, Pascal F.
APPLICANT: Maxgen, Inc.
TITLE OF INVENTION: Systems for Medicinal and Industrial Applications
TITLE OF INVENTION: Systems for Medicinal and Industrial Applications
FILE REFERENCE: 18097A-033510US
CURRENT APPLICATION NUMBER: US/09/892, 208A
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,161
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
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Sequence 51, Application US/10096550

GENERAL INFORMATION:

APPLICANT: Nolan, Garry P

APPLICANT: Nothenburg, Michael S.

TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR

TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR

TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR

TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR

CURRENT APPLICATION NUMBER: US/10/096,550

CURRENT APPLICATION NUMBER: 08/289,108

PRIOR FILING DATE: 1996-01-23

PRIOR FILING DATE: 1996-01-23

PRIOR FILING DATE: 1996-01-23

NUMBER OF SEQ ID NOS: 97

SEQTIMARE: PATENTIN VOIL OFF. 2.0

SEQ ID NOS: 97
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TYPE: PRT ORGANISM: Artificial Sequence PERTURE: OFFENTER: OFFENTER: OFFENTER: OFFENTER: OTHER INFORMATION: Sequence. OTHER INFORMATION: Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: synthetic. US-10-096-550-51
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                                                                                                                                                                                                                        Length 17;
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                                                                                                                                                                                                                      81.2%; Score 65; DB 6; Lk
100.0%; Pred. No. 0.00017;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 11; Conserv
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MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
05-09-740-876-1
                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (610)454-3816
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 1:
                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
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Best Local Similarity 83.3
Matches 10; Conservative
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TITLE OF INVENTION: VIRAL VECTORS AND THEIR USE FOR TREATING
HYPERPROLIFERATIVE DISORDERS, IN PARTICULAR RESTENOSIS
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10028247
GENERAL INFORMATION:
APPLICANT: Goldman, Stanley,
APPLICANT: Goldman, Stanley,
APPLICANT: Lathrop, Stephanie J.
APPLICANT: Lathrop, Pascal F.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Methods and Compositions for Developing Spore Display
TITLE OF INVENTION: Systems for Medicinal and Industrial Applications
TITLE OF INVENTION: Systems for Medicinal and Industrial Applications
TITLE OF INVENTION: Systems for Medicinal and Industrial Applications
TITLE OF INVENTION NUMBER: US, 050/24, 161
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 09/892, 208
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 0.0021;
0; Mismatches 2; Indels
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                                                                                                        ; OTHER INFORMATION: CotC27 including HAll epitope region US-09-892-208A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: CotC27 including HA11 epitope region US-10-028-247-2
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: Mail Drop 3C43, P.O. Box 5093
CITY: Collegeville
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09740876
GENERAL INFORMATION:
APPLICANT: BRANELLEC, Didier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WALSH, Kenneth
ISNER, Jeffrey M.
                                                                                                                                                                                        78.8%;
                                            TYPE: PRT ORGANISM: Bacillus subtilis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Bacillus subtilis
                                                                                                                                                                                      Query Match 78.8
Best Local Similarity 84.6
Matches 11; Conservative
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Matches 11; Conservative
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US-09-740-876-1
SEQ ID NO 2
LENGTH: 86
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ö ö Sequence 57, Application US/09415765A
GENERAL IRFORMATION:
APPLICANT: Anderson, David
TITLE OF INVENTION: Libraries
TITLE OF INVENTION: Libraries
TITLE OF ILING DATE: 1999-10-08
CURRENT APPLICATION NUMBER: US/09/415,765A
CURRENT APPLICATION NUMBER: 09/169,015
PRIOR APPLICATION NUMBER: 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ 1D NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 57
LENGTH: 19 Gaps Gaps ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-415-765A-57 ö ö COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/740,876
FILING DATE: 21-Dec-2000
CLASSIFCATION: CUNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/723,726
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: SAVILZKY, MARTIN R.
RECISTRATION NUMBER: 29,699
RECISTRATION NUMBER: 29,699
RECISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION: Length 14; Score 59; DB 5; Length 19; Pred. No. 0.0019; 0; Mismatches 2; Indels 2; Indels 73.8%; Score 59; DB 6; 83.3%; Pred. No. 0.0014; Live 0; Mismatches 2

us-09-284-787-2.rapn

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Query Match 73.8
Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity 71.4
Matches 10; Conservative
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; LOCATION: (1)..(26)
US-09-481-620A-34
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US-09-626-581C-57

Sequence 57, Application US/09626581C

Sequence 57, Application US/09626581C

GENERAL INFORMATION:
TITLE OF INVENTION: Tailor of Scaffold Proteins with Random Peptide
TITLE OF INVENTION: Libraries
TITLE OF INVENTION: Libraries
TITLE OF INVENTION: Libraries
CURRENT A-66900-37RMS

CURRENT FILING DATE: 1299-10-08

PRIOR FILING DATE: 1999-10-08

PRIOR FILING DATE: 1999-10-08

PRIOR FILING DATE: 1999-10-08

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 57

LENGTH. 19
Sequence 57, Application US/09626580B

GENERAL INFORMATION:
APPLICANT: Anderson, David
TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide
TITLE OF INVENTION: Libraries
TITLE OF INVENTION: Libraries
FILE REFERENCE: A-66900-2/RMS
CURRENT PELLING DATE: 2002-02-21
PRIOR PILLING DATE: 1998-10-08
PRIOR PILLING DATE: 1998-10-08
PRIOR PILLING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 63
SUSTWARE: Patentin Ver: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-626-581C-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59; DB 5; Length 19;
Pred. No. 0.0019;
0; Mismatches 2; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.8%;
83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity 83.3
Matches 10; Conservative
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US-09-481-620A-34
                                                                                                                                                                                                                                                                               SEQ ID NO 57
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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Sequence 33, Application US/10002244
GENERAL INPOMATION:
GENERAL INPOMATION:
THE OF INVENTION: Use of Heterologous Transcription Factors in Gene Therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Messer, Anne APPLICANT: Lecerf, Jean-Michel TITLE OF INVENTIONS METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS ETLE REFERENCE: INR-004CP CURRENT PRILING DATE: 2000-07-21 PRIOR APPLICATION NUMBER: 60/146,047 PRIOR APPLICATION NUMBER: 60/146,047 NUMBER OF SEO ID NOS: 45
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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APPLICANT: ARIAD Gene Therapeutics, Inc.
TITLE OF INVENTION: Rapamycin Based Regulation of Biological Events
FILE REFERENCE: 345 B PCT
CURRENT APPLICATION NUMBER: US/09/481,620A
CURRENT FILING DATE: 2000-01-12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 34
LENGTH: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: construct
US-09-620-9558-31
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Pred. No. 0.002
0; Mismatches
                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 12CA5epitope--SV40NLS
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CURRENT APPLICATION NUMBER: US/10/002,244
CURRENT FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31, Application US/09620955B GENERAL INFORMATION:
APPLICANT: Huston, James S.
                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          73.8%;
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71.4%;
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US-09-481-620A-24
; Sequence 24, Application US/09481620A
; Sequence 24, Application US/09481620A
; GENERAL INFORMATION:
    APPLICANT: ARIAD Gene Therapeutics, Inc.
; TITLE OF INVENTION: Rapemycin Based Regulation of Biological Events
; FILE REFERENCE: 345B PCT
; CURRENT APPLICATION NUMBER: US/09/481,620A
; CURRENT FILIO DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 24
: LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59; DB 6; Length 41;
Pred. No. 0.0044;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: 12CA5epitope--SV40NLS--ZFHD5'
NAME/KEY: PEPTIDE
LOCATION: (1) ...(41)
US-09-481-620A-24
SOFTWARE: Patentin version 3.0

SEQ ID NO 33

LENGTH: 27

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:

NAME/KEY: PEPTIDE

LOCATION: (1)..(27)

OTHER INFORMATION: PSMTN3

US-10-002-244-33
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Search completed: April 11, 2002, 10:21:36 Job time: 446 sec

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Run on:

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Roche Diagnostics GmbH
APPLICANT: Roche Diagnostics GmbH
TITLE OF INVENTION: Monoclonal Antibodies Against the Epitope YPYDVPDYA, A Process
TITLE OF INVENTION: Producing the Same and their Use
FILE REFERENCE: BMID9913US
CURRENT APPLICATION NUMBER: US/09/284,787
CURRENT FILING DATE: 1999-08-16
PRIOR APPLICATION NUMBER: PCT/EP97/05783
PRIOR FILING DATE: 1997-10-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
                                                                                  Sequence 4, Appli
Sequence 15, Appl
Sequence 13, Appli
Sequence 13, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 169, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 12, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 169, Appli
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                                  Sequence 7, Sequence 5
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ilarity 100.0%; Pred. No. 2.4e-05;
Conservative 0; Mismatches 0;
US-09-285-912A-68
PCT-USSO0-09002-11
PCT-USSO0-09002-11
US-09-134-793-7
US-09-134-793-7
US-09-134-793-7
US-09-134-793-7
US-09-134-793-7
US-09-134-793-7
US-09-134-793-7
US-09-134-793-11
US-08-10-24A-13
US-08-10-24A-13
US-08-10-24A-13
US-08-10-24A-13
US-08-10-24A-13
US-08-10-24A-13
US-08-10-24A-13
US-08-10-24A-13
US-08-10-24A-13
US-08-10-24B-14
US-08-10-24B-14
US-08-10-24B-16
US-09-10-24B-16
US-08-10-24B-16
US-08
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: ORGANISM: human influenza virus
US-09-284-787-3
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Best Local Similarity
Matches 13; Conserv
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US-08-787-738-51
   LENGTH: 13
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(without alignments)
13.533 Million cell updates/sec
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Sequence 1
Sequence 2
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-78-738-51
US-08-787-738-51
US-08-963-368-51
US-09-285-912-136
US-09-285-912A-130
US-09-285-912A-130
US-09-285-912A-130
US-09-285-912-130
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                                                                                                                                                                                                                                                                                                                    3148936 seqs, 277657034 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
                                                                                                                        April 11, 2002, 10:20:51
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Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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Result No.

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Score 67; DB 13;
Pred. No. 0.00068;
0; Mismatches 1;
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 91.7
Matches 11; Conservative
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US-09-285-912A-136
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                              APPLICANT: Notan, Garry P
APPLICANT: Notan, Garry P
APPLICANT: Rothenburg, Michael S.
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
TITLE OF INVENTION: PEPTIDES AND RNA MOLECULES
FILE REFERENCE: A-64259-1 correction
CURRENT APPLICATION NUMBER: US/08/787,738
CURRENT APPLICATION NUMBER: 08/589,108
PRIOR PLICATION NUMBER: 08/589,11
PRIOR PLICATION NUMBER: 08/589,911
PRIOR FILING DATE: 1996-01-23
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 51
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nolan, Garry P
APPLICANT: Nolan, Garry P
APPLICANT: Nothenburg, Michael S,
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
TITLE OF INVENTION: DEPTIDES AND RNA MOLECULES
FILE REFERENCE: A-64259-1 COLTECTION
CURRENT APPLICATION NUMBER: US/08/787,738B
CURRENT APPLICATION NUMBER: 08/589,108
PRIOR FILING DATE: 1996-01-23
PRIOR PLICATION NUMBER: 08/589,911
PRIOR PLICATION NUMBER: 08/589,911
PRIOR FILING DATE: 1996-01-23
NUMBER OF SEO ID NOS: 97
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 51
LENGTH: 17
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US-08-787-738-51
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US-08-787-738B-51
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Pred. No. 0.00068;
0; Mismatches 1; Indels
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Pred. No. 0.00068;
0; Mismatches 1;
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US-08-787-738B-51

Sequence 51, Application US/08787738B

; CENERAL INFORMATION:
Sequence 51, Application US/08787738
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; GENERAL INFORMATION:
; APPLICANT: Nolan, Garry P
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91.7%;
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Best Local Similarity
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Best Local Similarity
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US-08-963-368-51
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TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRA-CELLULAR
TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES
FILE REPERBENCE: A-64250-2/DJB/RNS/DR
CURRENT APPLICATION NUMBER: US/08/963,368
CURRENT FILING DATE: 1997-11-03
PRIOR PILICATION NUMBER: 08/589,108
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1997-01-23
NUMBER OF SEQ ID NOS: 102
SEQ ID NOS: 102
SEQ ID NO 51
LENGTH: 17
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PAPLICANT: CARACTERION:
DAVID

TITLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES FILE REFERENCE: A - 66103 - 1,004 PRASS, STR

CURRENT APPLICATION NUMBER: US/09/285,912

CURRENT FILING DATE: 1999-04-02

NUMBER OF SEQ ID NOS: 150

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 136

LENGTH: 18
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GENERAL INFORMATION:
APPLICANT: Anderson, David
TITLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES
FILE REPERENCE: A-66103-1/JDB/RMS/SJR
CURRENT APPLICATION UNMBER: US/09/285,912A
CURRENT FILING DATE: 1999-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: epitope tag
; OTHER INFORMATION: sequence.
US-08-963-368-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-285-912-136
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Pred. No. 0.00073;
0; Mismatches 1; Indels
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Gaps
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TITLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES
FILE REPERENCE: A -66103-1/DJB/RMS/SJR
CURRENT APPLICATION NUMBER: US/09/285,912
CURRENT FILING DATE: 1999-04-02
PRIOR REPLICATION NUMBER: 60/080,444
PRIOR RILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin Ver. 2.0
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PAPLICANT: Anderson, David

TITLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES

FILE REFERENCE: A-66103-1/201B/RMS/SJ85, 912A

CURRENT APPLICATION NUMBER: US/09/285, 912A

CURRENT FILING DATE: 1999-04-02

PRIOR FILING DATE: 1998-04-02

NUMBER OF SEQ ID NOS: 150

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 68

LENGTH: 38
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US-09-285-912A-68
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Pred. No. 0.0018;
0; Mismatches 1; Indels
                                                      1; Indels
                                                      0; Mismatches
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                                                                                                                                                                                                                  ; Sequence 68, Application US/09285912
; GENERAL INFORMATION:
                89.3%;
91.7%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7
Matches 11; Conservative
                  Query Match 89.3
Best Local Similarity 91.7
Matches 11; Conservative
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Best Local Similarity
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US-09-285-912-68
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LENGTH: 38
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TITLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES
FILE REFRENCE: A -66103-1/D16RMS/SJR
CURRENT APPLICATION NUMBER: US/09/285,912
CURRENT FILING DATE: 1999-04-02
PRIOR FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PALENCIN Ver. 2.0
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-285-912A-136
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Pred. No. 0.00073;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                    89.3%;
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91.7%;
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                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 91.7
Matches 11; Conservative
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Matches 11; Conservative
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US-09-285-912A-130
                                                      SEQ ID NO 136
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APPLICANT: DOWDY, STEVEN F
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   protein
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Best Local Similarity
Matches 11; Conserv
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   ; MOLECULE TYPE:
PCT-US98-16887-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109
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US-09-134-793-7
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              Sequence 11. Application PC/TUS0009002
GENERAL INFORMATION:
FEDERAL INFORMATION:
TITLE OF INVENTION: Anti-apoptchic fusion polypeptide
FILE REFERENCE: 150.195w01
CURRENT FILING DATE: 2000-04-07
EARLIER APPLICATION NUMBER: US 60/128,021
EARLIER FILING DATE: 1999-04-06
EARLIER FILING DATE: 1999-04-05
SEALLER FILING DATE: 1999-04-05
SOFTWARE: FILING DATE: 1999-04-05
SOFTWARE: FILING DATE: 1999-04-05
SOFTWARE: FILING DATE: 1999-04-05
SOFTWARE: FASTER FOR WINDOWS VERSION 4.0
SEQ ID NO 11
LENGTH: 16
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APPLICANT: Washington University
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman,
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                       Score 65; DB 1;
Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 47275-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US98/16887
                                                                                                                                                                                                                                                                                                                                                                                          86.7%; Scor.
100.0%; Pre
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APPLICATION NUMBER: 60/056,713
FILING DATE: 22-AGG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: pTAT-HA linker PCT-US00-09002-11
                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
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TOPOLOGY: linear
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Best Local Similarity
Matches 11; Conserva
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CLASSIFICATION:
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PCT-US00-09002-11
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PCT-US98-16887-7
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Score 65; DB 1; Length 10, Pred. No. 0.0014;
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                                                                                                                                                                                                               Sequence 7, Application US/09134793
GENERAL INFORMATION:
APPLICANT: Dowdy, Steven F.
APPLICANT: Jessee, Joel A.
TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 15; L4
Pred. No. 0.0014;
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SOFTWARE: FSASESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,793
   86.7%; Scc...
100.0%; Pred. No. ...
0; Mismatches
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100.0%; Pred. No. v...
0; Mismatches
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US-09-134-793A-7
Sequence 7, Application US/09134793A
; GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNBER: 60/056
FILING DATE: 22-AUG-1997
ATTORREY/AGENT INFORMATION:
NAME: COTLESS, PETER F
REGISTRATION NUMBER: 33,86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
                 Query Match 86.7
Best Local Similarity 100.
Matches 11; Conservative
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FEATURE:
OTHER UNFORMATION: Amino acid sequence of ptat-HA plasmid linker sequence
US-09-300-639B-4
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; OTHER INFORMATION: Description of Artificial Sequence: pTAT-HA linker
US-09-134-793A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-300-639B-4

Sequence 4, Application US/09300639B

Sequence 4, Application US/09300639B

GENERAL INFORMATION:

APPLICANT: Steven F. Dowdy

TITLE OF INVENTION: Methods for Transducing Fusion Molecules

FILE REFERENCE: 48031

CURRENT APPLICATION NUMBER: US/09/300,639B

CURRENT FILING DATE: 1999-04-27

PRIOR PLILING DATE: 1998-04-28

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

LENGTH: 16
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APPLICANT: JESSEE, JOEL A.

TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM AND USE THEREOF
FILE REPERBENCE: 1742/47275
CURRENT APPLICATION NUMBER: US/09/134,793A
CURRENT FILING DATE: 1998-08-14
NUMBER OF SEC ID NOS: 9
SOFTWARE: Patentin Ver: 2.1
SEC ID NO 7
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 86.7%; Score 65; DB 15; Length 16; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
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Search completed: April 11, 2002, 10:20:51 Job time: 401 sec

2 SGYPYDVPDYA 12

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Sequence 51, Application US/09916940
GENERAL INFORMATION:
APPLICANT: NOLAN, GARTY P
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
FILE REFERENCE: A-64260-6/RMS/AMS
CURRENT FILING DATE: 2000-10-29
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1996-01-23
                                             Gaps
    Sednence Sed
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US-09-453-234-80
US-09-481-620A-34
US-09-481-620A-34
US-10-002-244-35
US-09-892-208A-24
US-10-002-244-25
US-09-852-370A-65
US-10-041-264A-9
US-10-041-264A-9
US-10-041-30A-9
US-10-041-30A-9
US-10-041-30A-9
US-10-041-30A-9
US-09-31-31A-24
US-09-31-31A-24
US-09-180-167A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQUENCE 8, Application US/09896915
GENERAL INFORMATION:
APPLICANT: Medical Research Council
APPLICANT: Grifiths, Andrew
TITLE OF INVENTION: Optical Sorting Method
FILE REFERENCE: 18396/2022
CURRENT APPLICATION NUMBER: US/09/896,915
CURRENT FILING DATE: 1999-01-07
PRIOR APPLICATION NUMBER: GB9900298.2
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: CB9900298.2
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTING DATE: 340
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; ORGANISM: plasmid pET-23d(FLAGHA)
US-09-896-915-8
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92.38;
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Best Local Similarity 92.3
Matches 12; Conservative
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US-09-916-940-51
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US-09-896-915-8
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USOG_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/USO0_NEW_COMB.pep:*
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-775-052A-15

US-09-775-052A-16

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US-09-453-234-76

US-09-453-234-84

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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SOFTWARE: Patentin Ver. 2.0
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US-09-626-580B-57
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TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
TITLE OF INVENTION: PEPTIDES AND RNA MOLECULES
FILE REFERENCE: A-6425-1 correction
CURRENT FILING DATE: 2002-03-12
PRIOR PAPLICATION NUMBER: 08/70/096,550
PRIOR APPLICATION NUMBER: 08/70/738
PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PATENTIN VET: 2.00
SOFTWARE: PATENTIN VET: 2.00
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TITLE OF INVENTION: Eusions of Scaffold Proteins with Random Peptide
TITLE OF INVENTION: Libraries
FILE REFERENCE: A66900-17RMS/SJR
CURRENT APPLICATION NUMBER: US/09/415,765A
                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: epitope tag
OTHER INFORMATION: sequence.
US-09-916-940-51
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US-10-096-550-51
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      PRIOR FILING DATE: 1996-01-23
PRIOR APPLICATION NUMBER: US 08/789,333
PRIOR FILING DATE: 1997-01-23
PRIOR PLLING DATE: 1997-01-23
PRIOR FILING DATE: 1997-01-23
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 51
PRIOR APPLICATION NUMBER: US 08/589,911
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8.02-09-415-765A-57
5. Sequence 57, Application US/09415765A
6. GENERAL INFORMATION:
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; APPLICANT: Nolan, Garry P
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 91.7
Matches 11; Conservative
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US-10-096-550-51
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GENERAL INFORMATION:
APPLICANT Anderson, Day
TILLE OF INVENTION:
TILLE OF INVENTION:
LIDRATION LIDRATES
FILE REFERENCE: A-66900-2/RMS
CURRENT APPLICATION NUMBER: U3/09/626,580B
CURRENT FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 57
LENGTH: 19
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GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Anderson, David
TITLE OF INVENTION: Exions of Scaffold Proteins with Random Peptide
TITLE OF INVENTION: Libraries
FILE REFERENCE: A-66900-37RMS
CURRENT APPLICATION NUMBER: 09/09/626,581C
CURRENT PILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/169,015
PRIOR APPLICATION NUMBER: 09/169,015
PRIOR APPLICATION NUMBER: 09/4169,015
PRIOR APPLICATION NUMBER: 09/4169,015
PRIOR PILING DATE: 1998-110-08
PRIOR FILING DATE: 1999-110-08
PRIOR POPLICATION NUMBER: 09/415,765
PRIOR POPLICATION NUMBER: 09/415,765
PRIOR POPLICATION NUMBER: 09/415,765
PRIOR APPLICATION NUMBER: 09/415,765
PRIOR APPLICATION NUMBER: 09/415,765
                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-415-765A-57
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Pred. No. 0.0001;
0; Mismatches 1; Indels
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Pred. No. 0.0001;
0; Mismatches 1; Indels
CURRENT FILING DATE: 1999-10-08
PRIOR APPLICATION UNMBER: 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 63
SOFWRARE: Patentin Ver: 2.0
SEQ ID NO 57
LENGTH: 19
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative (
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91.7%;
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Best Local Similarity 91.7°
Matches 11; Conservative
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83.3%; Pred. No. 0.013;
ive 0; Mismatches 2; Indels
  Length 16;
                                             Indels
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ch 86.7%; Score 65; DB 6; Lv Similarity 100.0%; Pred. No. 0.00018; 11; Conservative 0; Mismatches 0;
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Pred. No. 0.013;
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: GTay, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Genebar, Nis
APPLICANT: GORDHAR, INTENDATIONAL
CURRENT BLOSICE DISGNOSTICS, Inc.
APPLICANT: GORDHAR, 10001005
TITLE OF INVENTION: HUMAN ANTIDOGIES
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 36
LEWATH: 24
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Sequence 40, Application US/09453234

GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Gary, Jeff
APPLICANT: Conberg, Nis
APPLICANT: Genebarm international
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION: HUMBER: US/09/453,234
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT APPLICATION NUMBER: US/09/453,234
SOURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US/09/453,234
SOURWARE: PATENTING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 112
SEQ ID NO 40
LEWATH: 224
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83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity 83.3
Matches 10; Conservative
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COTHER INFORMATION: M1-4L
US-09-453-234-40
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ORGANISM: Homo sapiens
US-09-453-234-36
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GENERAL INFORMATION:
APPLICANTON:
APPLICANTON:
ATTLE OF INVENTION:
FILE REFERENCE: 48881/1742
CURRENT APPLICATION NUMBER: US/09/775,052
CURRENT FILING DATE: 1998-112-10
PRIOR PELICATION NUMBER: 09/208,966
PRIOR FLILING DATE: 1998-112-10
PRIOR FLILING DATE: 1998-112-10
PRIOR FLILING DATE: 1998-04-20
PRIOR FLILING DATE: 1998-04-20
PRIOR FLILING DATE: 1998-04-20
PRIOR FILING DATE: 1997-12-10
PRIOR FILING DATE: 1997-12-10
NUMBER: OF SEQ ID NOS: 57
SOFTWARE: PALCHAIL VET. 2.0
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GENERAL INFORMATION:
APPLICANT: Dowdy, Steven F,
TITLE OF INFORMATION:
TITLE OF INFORMATION:
CURRENT APPLICATION NUMBER: US/09/775,052A
CURRENT FILING DATE: 2011-12-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PALCHIN Ver. 2.0
                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-626-581C-57
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Pred. No. 0.0001;
0; Mismatches 1; Indels
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                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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91.7%;
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Best Local Similarity 91.7
Matches 11; Conservative
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: human
US-09-775-052A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: human
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  SEQ ID NO 57
LENGTH: 19
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Pred. No. 0.013;
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Pred. No. 0.013;
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                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/453, 234 CURRENT FILING DATE: 1999-12-01 PRIOR APPLICATION NUMBER: US 60/157,415 PRIOR FILING DATE: 1999-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 52
LENGTH: 224
                                                                                        GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-0001100s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 52, Application US/09453234
Sequence 52, Application US/09453234
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Blosite Diagnostics, Inc.
APPLICANT: Blosite Diagnostics, Inc.
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
                                                       US-09-453-234-48; Sequence 48, Application US/09453234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.3%;
83.3%;
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83.3%;
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48
LENGTH: 224
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) OTHER INFORMATION: M1-21L
US-09-453-234-48
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83.3%; Pred. No. 0.013;
ive 0; Mismatches 2; Indels
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Pred. No. 0.013;
0; Mismatches 2; Indels
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                                                                                                                                                                     APPLICANT: Buechler, Joe
APPLICANT: Buechler, Joe
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Genebarm International
TITLE OF INVENTION: Human Antibodies
TITLE REFERENCE: 020015-000110US
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
SENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMY: Buechler, Joe
APPLICAMY: Valkirs, Gunars
APPLICAMY: Valkirs, Gunars
APPLICAMY: Lonbergy, Nils
APPLICAMY: Lonbergy, Nils
APPLICAMY: GenPharm International
TITLE OF INVENTION: Human Antibodies
TITLE OF INVENTION: Human Antibodies
TITLE FEFRENCE: 020015-0001100S
CURRENT FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 46
LENGTH: 224
                                                                                                                                      Sequence 44, Application US/09453234 GENERAL INFORMATION:
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Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity 83.3
Matches 10; Conservative
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US-09-453-234-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-8L
US-09-453-234-44
                      2 GSGYPYDVPDYA 13
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US-09-453-234-44
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RESULT 15

Squence 76, Application US/09453234

Squence 76, Application US/09453234

GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Buechler, Joe
APPLICANT: Buechler, Joe
APPLICANT: Bloste Diagnostics, Inc.
APPLICANT: Cenpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-0001100S
CURRENT FILING DATE: 1999-12-01
PRIOR FILING D
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12CA5 epitope of m Murine signalling Influenza haemagal 12CA5 epitope of h Human PAR-2 12CA5 Influenza haemaggluthin tag Chimeric adenovira

Influenza virus ha Peptide sequence o

Human influenza vi Binding domain of Haemagglutinin epi CTLA 4 VLD CDR loo FLAG peptide from Haemagglutinin ant

HA-tag peptide. U Murine signalling Peptide comprising

Perfect score:

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Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Max-interacting polypeptide and DNA encoding them - used as anticancer agents and to screen for agents which inhibit cellular proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Max-interacting protein; plasmid pJG4-5; fusion protein; cancer; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                               AAW60722
AAW59450
AAW46333
AAY31722
AAY39621
                                                                                                                                                               AAY06463
AAY25085
AAW92477
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AAY79580
AAB61542
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AAB10960
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AAB29033
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AAB14332
AAY96884
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                                                                                                                                                      AAY26291
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR56545 standard; Protein; 9 AA
93WO-US12643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9305-0011398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEHO ) GEN HOSPITAL CORP.
 WPI; 1994-264033/32.
Hal epitope tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-1993;
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 AAR56545;
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Hydrophilic peptid
Epitope for anti-H
Transforming growt
Haemagglutinin epi
pJG4-5 library pla
Purlication tag o
Influenza virus ha
10-mer peptide tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hal epitope tag.
Viral antigenic ep
HA-epitope tag. S
                                                                        / Search time 53.05 Seconds
(without alignments)
12.567 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                              **Sinssy_geneseq_geneseqp_AA1980_DAT:**

**Sinssy_gedata_geneseq_geneseqp_AA1981_DAT:**

**Sinssy_gedata_geneseq_geneseqp_AA19
                                                                                                                                                                                                                        522463
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                522463 seqs, 74073290 residues
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                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR78372
AAW03654
AAR92029
AAW27096
AAW00970
AAW01651
AAW01661
                                                      OM protein - protein search, using sw model
                                                                         April 11, 2002, 10:14:10
                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match 1
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26439

Disclosure; Page 43; 57pp; English.

Influenza haemaggl HA epitope, SEQ ID Haemagglutinin epi Influenza virus HA C-terminal influen

Murine signalling Amino acid sequenc Influenza hemagglu

Haemagglutinin epi 12CA5 antibody pep

Influenza hemaglut HA tag, SEQ ID NO: SNP detection meth

Haemagglutinin epi HA residues used 1 Influenza hemaglut

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Sequence

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This sequence represents a viral antigenic epitope of influenza virus haemagglutinin. The DNA sequence encoding this antigen may be included into a modified tobacco mosale virus (TMV) coat protein gene or a modified movement gene. The modified infectious clone is used to transfect a plant which is then cultured such that the epitope may be recovered from the leaves. The epitope coding sequences are included into the coat protein or movement protein genes such that the translated product contains one or more amino acids immediatly adjacent to the epitope that are readily treated chemically or enzymatically to release to peptide epitope from the precursor protein. Recombinant viruses the peptide epitope from the precursor protein. Recombinant viruses containing modified movement or coat proteins may be used in the method of the invention for the overproduction of heterologous proteins. The method is esp. used for the production of heterologous proteins. The method is esp used for the production of peptides which cause an antibod in mammals, partic. for use in viral vaccines, or for generating a contraceptive immune response. The infectious clones may encode coat proteins for other plant viruses, or proteins conferring protection against insects and diseases.
                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Truncated, tobacco mosaic virus; TMV; movement protein; coat protein; frame shift; mutation; in-frame stop codon; antigen; mammal; viral vaccine; contraceptive; immune response; plant virus; insect.
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viral antigenic epitope of influenza virus haemagglutinin (12CA5)
                                     nuclear localization sequence (AAR56544), the B42 acid blob transcriptional activation domain and the HA1 epitope tag is expressed from pJG4-5-1. Mxi (and sense/antisense RNA) can be delivered to e.g. bone marrow as therapeutic agents for cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Overprodn. of heterologous peptide in plants via tobacco mosaic virus infection - in which the coat protein gene is modified by insertion of heterologous sequence, partic. for producing viral
                                                                                                                                                                                                                                             ;
                    Max-interacting (Mxi) protein fusion protein with the SV40
                                                                                                                                                                                                   Length 9;
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                                                                                                                                                                                                 Score 55; DB 15;
Pred. No. 4.3e+05;
Mismatches 0;
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                                                                                                                                                                                                                      Local Similarity 100.
nes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-283768/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HA-epitope tag; affinity tail; FADD; Fas receptor; binding; Fas-associating protein with novel death domain; apoptosis; gene therapy; antibody; immunoassay; drug screening; diagnostic; AIDS; antiinflammatory; antitumour; cerebroprotective;
                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FADD protein that binds to cytoplasmic region of Fas receptor identifying inhibitors of Fas-associated apoptosis useful for treating e.g. AIDS, leukaemia, stroke, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This HA-epitope tag peptide has been fused to a FADD protein
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100.0%; Score 55; DB 16; 100.0%; Pred. No. 4.3e+05;
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                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                       AAW03654 standard; Peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0443982.
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                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dixit VM, O'Rourke K;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroprotective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HA-epitope tag.
                                                                                                                                   1 YPYDVPDYA
                                                                                                                                                                         WO9631603-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-0CT-1996,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW03654;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                     Matches
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This peptide comprises an epitope for an anti-haemagglutinin (HA) tay monoclonal antibody. It can be included in the sequence of a recombinant G protein-coupled receptor that is activated superiorly by a synthetic ligand, i.e. a RASSL (see AAW30298 and AAW30299), to facilitate ease of detection and purification. RASSLs are used in a novel method for selectively activating a target cell, providing direct, selective control of cellular proliferation, especially for amplification of transfected cells during gene therapy procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Selective activation of target cell expressing modified G protein coupled receptor - allows control of cellular proliferation, especially for amplification of transfected cells in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transforming growth factor-beta activated kinase epitope HA-TAKI.
                                                                                                    Selective target cell activation; G protein-coupled receptor; RASSL; gene therapy; cell proliferation; haemagglutinin; HA tag; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGF-beta; signal transmission; TGF-beta activated kinase; MAPK kinase activator; AMK-1; bone morphogenetic protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 55; DB 18;
100.0%; Pred. No. 4.3e+05;
ive 0; Mismatches 0;
                                                                     Epitope for anti-HA tag monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 57; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW27094 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                 97WO-US05334
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                                  14-APR-1998 (first entry)
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Best Local Similarity 100.

Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein kinase; epitope.
                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-502739/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YPYDVPDYA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP09163990-A.
                                                                                                                                                                                                                                                                                               25-MAR-1997;
                                                                                                                                                                                                                                                                                                                                  26-MAR-1996;
                                                                                                                                                                                                                     WO9735478-A1
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                                                                                                                                                                                                                                                                                                                                                                                                             Conklin BR;
                                                                                                                                                                                    Synthetic.
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AAW30296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides contain a first portion of 5-99 amino acids joined to a second portion contg. at least a functional domain of epimorphin. The first portion may be selected from the peptides given in AAR92029 to AAR92036. The second portion may be full-length epimorphin (see AAR92037 to AAR92042 for human and mouse epimorphins). Fragments of epimorphins given in AAT16083 to AAT16090 are used in the produ. of modified epimorphins. The modified epimorphins are useful for the development of diagnosis and treatment of morphogenetic abnormalities of epithelial tissue or novel remedies for wounds, eg burns, after surgery and for artificial organs. They may also be used as components of cosmetics, hair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptide containing an epimorphin functional domain - has possible benefits in epithelial tissue treatments, e.g. burns and for artificial organs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                   Epimorphin; human; mouse; wound; burn; epithelial tissue; diagnosis; treatment; morphogenetic abnormality; cosmetic; hair growth stimulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
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                                                                                                                                                                                                                                                          Hydrophilic peptide for epimorphin modification (1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 55; DB 17;
100.0%; Pred. No. 4.3e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW30296 standard; Peptide; 9 AA.
                                                                                                                                             AAR92029 standard; peptide; 9 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95JP-0099980.
94JP-0162874.
95JP-0099979.
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                                                                                                                                                                                                                       (first entry)
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth stimulators, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koshida S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-118213/13.
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               1 YPYDVPDYA
                                31-MAR-1995;
21-JUN-1994;
31-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-1995;
                                                                                                                                                                                                                     29-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                AAR92029;
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Length 9;

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WO9640767-A2
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                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                               The present sequence represents an epitope, HA-TAK1, of transforming growth factor-beta (TGF-beta) activated kinase, TRK-1. The DNA encoding TAK-1 is used to produce the TAK-1 protein which is involved in the TGF-beta family signal transmission system. TAK-1, also known as activator of MAPK Kinase (AMK-1), is an enzyme which is activated kinase by phosphorylation.
                                                                                     DNA encoding transforming growth factor-beta-activated kinase, TAK-1 - useful for studying the TGF-beta signal transmission system
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid binding proteins - having an acidic amino acid sequence extension at the amino-terminus, to increase ability to regulate gene transcription, useful e.g. in cancer therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                       acidic extension peptide; gene control; gene regulation; transcription; dominant negative protein; cancer; drug therapy; drug design; EBP; leucine zipper; haemagglutinin.
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                                                                                                                                                                                                                                                                                                                                                                                                DNA binding protein; RNA binding protein; amphipathic peptide;
                                                                                                                                                                                                                              DB 18; Length 9;
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                                                                                                                                                                                                                                       4.3e+05;
                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                              Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEALTH & HUMAN SERVICES.
                                                                                                                Example 4; Page 8; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                            AAW00970 standard; Peptide; 9 AA
                                                                                                                                                                                                                             100.0%; 100.0%; E
                                          (CHUS ) CHUGAI PHARM CO LTD. (UENO/) UENO N.
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96JP-0256747
                 96US-0685625
95JP-0253549
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96US-0018496
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                      Similarity 100.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                               Haemagglutinin epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krylov D, Vinson CR;
                                                                    WPI; 1997-380171/35
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(VINS/) VINSON C R.
                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRYL/) KRYLOV D.
                                                                                                                                                                                                     9 AA;
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27-SEP-1996;
                 24-JUL-1996;
29-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                            AAW00970;
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                                                                                                                                                                                                                                               Matches
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The present sequence represents the HAI epitope tag of the pJG4-5 library plasmid used during the isolation of the E6AP-binding proteins. E6AP mediates ubiquitination and so the inactivation of e.g. p53 tumour suppressor. The E6AP-binding protein is likely to be involved in normal cell homeostasis and in the pathogenesis of proliferative and differentiation disorders, e.g. regulation of gene expression or the cell cycle, modification of cell surface receptors, biogenesis of ribosomes and DNA repair. The protein, which can optionally be generated in vivo by gene thrapy, may useful in treatment and prevention of papilloma virus infected transformed cells and carcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ubiquitination; p53; tumour suppressor; homeostasis; papilloma virus; epithelial cell; acne; icthyosis; aphthous ulcer; hair growth; antibody; cell proliferation.
                                                                                                                                                                                                                                                                                            regulators of gene transcription, cell growth and cell proliferation They can be used in cancer therapeutics, to treat diseases caused by eukaryotic microorganisms or by viruses, and as tools for drug development, rational drug design, and drug and gene therapies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                      This peptide sequence comprises a haemagglutinin epitope that can be attached to the N-terminus of a nucleic acid binding protein (NABP) such as a leucine zipper bZIP protein or bHLH protein. Claimed NABPs having an appended acidic extension peptide (see AAW00958-65) can regulate the function of a target nucleic acid or gene to which they are bound, and act as potent dominant-negative.
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for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 55; DB 18;
ilarity 100.0%; Pred. No. 4.3e+05;
Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pJG4-5 library plasmid HA1 epitope tag.
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Claim 16; Page 58; 144pp; English.
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Best Local Similarity
Matches 9; Conserv
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Thu Apr 11

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and may also be used to regulate epithelial cell processes more generally, e.g. in cases of psoriasis, acne, icthyosis, aphthous ulcers. It may also be used to control wound healing, and inhibit growth of hair. It can also be used to generate antibodies which are used in immunoassays to determine the protein levels. The encoding nucleic acid as be used to prepare recombinant proteins and oligonucleotides useful as probes and primers for diagnostic detection of (mutant) mRNA for the protein in (transformed) cells, also for antisense therapy. It can also be used for the detection of mutations in EGAP-binding protein-encoding genes, mis-expression of these genes or mis-incorporation of the protein assess risk of disorders characterised by cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. The present sequence represents a specifically claimed purification tag. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag:proteinase site:ECM binding site:proteinase site:TGF-beta. TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion
                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transforming growth factor-beta fusion protein; wound healing; artificial skin; surgery recovery time.
                                                                                                                                                                                                                                                             Length 9;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                             Score 55; DB 18;
Pred. No. 4.3e+05;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purification tag of a TGF-beta fusion protein.
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                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          AAWO8162 standard; Peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 44; 59pp; English.
                                                                                                                                                                                                                                                             100.0%;
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHEUNG D T.
HALL F L.
NIMNI M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-043065/04.
N-PSDB; AAT42766.
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                                                                                                                                                                                                              9 AA;
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                                                                                                                                                                                                                                                                                                                                                05-JUN-1996;
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(NIMN/)
(TUAN/)
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of a purification tag facilitates purification of the fusion protein. The proteinses site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta required to be administered to be effective and reduces the concentration of circulating TGF-beta which may result in undesirable effects.
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A DNA sequence encoding an influenza virus haemagglutinin (HA) epitope tag (AAM12385) and the murine Ig kappa-chain V-Jz-C region signal peptide (AAM12384) was subcloned from a single chain antibody (SFV) contg. vector (pCR3.2) as an ECORV-Sall fragment and ligated with ECORV/Sall-digested pCR3.1.1. The resulting vector was used in the construction of eukaryotic expression vector pPhOx. TM (see also AAT63235). Expression of the HA epitope tag allowed detection of the expressed sFV by monoclonal antibody 12CA5. Vector pPhOx.TM is used in novel methods for the identification and isolation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pPhOx.TM; eukaryotic expression vector; transfected cell; single chain antibody; sFv; molecular hook; haemagglutinin; epitope tag.
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                                                                                                                                                                                          100.0%; Score 55; DB 18;
100.0%; Pred. No. 4.3e+05;
ive 0; Mismatches 0;
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100.0%; Pred. No. 4.3e+05;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transfected cells from total cell population
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Influenza virus haemagglutinin epitope tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 27; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chang M,
                                                                                                                                                                                                                                                                                                                                                                     AAW12385 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transfected eukaryotic cells
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                                                                                                                                                                                                                           9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bernhard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-179169/16.
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les 9; Conserv
                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                        1 YPYDVPDYA 9
                                                                                                                                             9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Influenza virus.
                                                                                                                                                                                                                                                                          18-JUN-1997
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Best Local S:
Matches 9
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This represents an in-frame 12CA5 peptide epitope of the alpha chain of mouse leukaemia inhibitory factor (LIF) receptor (LIFR). The invention relates to interspecies LIFR alpha-chain chimeras. The chimeric polypeptide comprises (i) a heamopoietin domain, linked, bound or associated with (ii) an immunoglobulin (Ig)-like domain, such that the chimera can bind cytokines. The chimeric polypeptide specifically binds LIF, so is used to treat conditions that require antagonism of LIF, specifically inflammation, but more generally may be designed to bind other cytokines such as interleukins and colony-stimulating factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Induction; intracellular aggregation; cytoplasmic tail; zeta chain; T cell receptor/CD3 complex; signal; transcription; reporter gene; homodimerization; Fas receptor; cell-specific apoptosis; Gall4; VPl6; heterodimerization; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide containing haemopoietin domain and immunoglobulin-like domain - also related nucleic acid, binds cytokines, specifically leukaemia inhibitory factor, and is used to
                                                                                                                                                                                                             LIFR, leukaemia inhibitory factor; LIF; interspecies; chimeric; haemopoietin domain; immunoglobulin; cytokine; interleukin; colony-stimulating factor; mouse; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metcalf D, Nicola NA, Owczarek CM, Zhang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 19; 100.0%; Pred. No. 4.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                      12CA5 epitope of mouse LIFR alpha-chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 24; 58pp; English.
                                        AAW81556 standard; peptide; 9 AA.
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Best Local Similarity
' has 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treat inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-1998;
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                                                                                                                            04-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-1998
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                                                                                 AAW81556;
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RESULT 12
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                    AAW81556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant antibodies capable of binding to two different antigenic sites, contain Fab fragments from the same or, pref, different antibodies, which are brought into association by complementary antibodies, which are brought into association by complementary interactive domains, esp. leucine zipper domains, which have been inserted into a region of the antibody heavy chain constant region. Recombinant proteins c-fos LZ/Fab OKT2 and c-jun LZ/Fab OKT3 showed ittle or no binding to normal lymphocytes when analysed individually but bound very clearly to the cells when mixed to form a homodimeric antibody. The labelled antibodies are useful for detecting a selected antigen (bound by the first or second Fab) in a biological sample or treatment of cancer and viral infections. AAW01661 is a 10-mer peptide tag derived from Influenza haemagglutinin. DNA encoding the 10-mer was cloned into lambda HC2 to provide a peptide tag which will be present on the heavy chain cloned into pHC2.
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                                                                                                                                                                                                                                                                                                                                         monoclonal; recombinant; antibody; bispecific; antigenic site;
Fab fragment; complementary interactive domain; leucine zipper;
c-fos; c-jun; treatment; cancer; viral infection; primer; PCR;
polymerase chain reaction; amplification; peptide tag.
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                                                                                                                                                                                                                                                                                                   10-mer peptide tag derived from Influenza haemagglutinin.
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100.0%; Pred. No. 4.3e+05;
iive 0; Mismatches 0;
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                                                                                                                                                                    AAW01661 standard; Peptide; 9 AA
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90US-0622983.
91WO-US09019.
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Best Local Similarity
9; Conserve
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                  1 YPYDVPDYA
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04-DEC-1990;
03-DEC-1991;
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Curtis PJ;

Seguence

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Synthetic.

AAW01661;

AAW01661 RESULT

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Gaps

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Length 9; Indels

Mus sp.

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This peptide comprises the influenza virus haemagglutinin epitope. A synthetic oligonuclectide (see AAV07684) encoding the epitope has been inserted into plasmid pyun563 (see AAV07706), which contains DNA encoding Mycobacterium tuberculosis recA inteln (see also AAV07705) inserted into an aph selectable marker gene and includes an internal BglII site. E. coli transformants showed a high splicing frequency. The invention provides novel vector constructs that include a DNA sequence encoding an inteln inserted into a selectable marker gene such as aph. DNA of interest can be cloned into a unique restriction site of the inteln, and the vector used as a vaccine or transformed into a vaccine vector. The vectors may also be used in methods of selecting translated open reading frames or genes, leading to the identification of protective antigens of
                                                                                                                                                          New vector constructs for selection of open reading frames - comprise origin of replication and DNA sequences encoding selectable marker, intein and regulatory elements for expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemagglutinin 12CA5 epitope; polyclonal rabbit antibody HA.11; human betal-adrenergic receptor; betal-AR; transgene; heart tissue-specific promoter; transgenic animal model; heart muscle disease; heart failure.
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                                                    (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
                                                                                                                                                                                                                                        Disclosure; Fig 7; 83pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12CA5 epitope of haemagglutinin.
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                                                                                         Daugelat S, Jacobs WR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-1997;
               13-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bristow MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-0CT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW80131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW76736-w76764 are peptides used to design primers used in a novel method for inducing a biological process in a cell. The method can be used to induce the intracellular aggregation of the cytoplasmic tail of the zeta chain of the T cell receptor/CD3 complex, leading to signalling and transcription of a reporter gene. The method also has applications for the homodimerization of the cytoplasmic tail of the Fas receptor, leading to cell-specific apoptosis and for the heterodimerization of Gald and VP16, leading to direct transcription of a reporter gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inducing a biological process in a cell using ligand-induced gene expression for e.g. cell death - using DNA construct encoding ligand-binding domain and dimerisable protein domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Intein; reck; DNA repair enzyme; vaccine; vector; antigen; open reading frame; haemagglutinin.
                                                                                                                                                                                                                                                                                                                                                                         Spencer DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 55; DB 19; ilarity 100.0%; Pred. No. 4.3e+05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                       Crabtree GR, Schreiber SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 71-72; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Influenza haemagglutinin epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW66198 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                  ) UNIV LELAND S STANFORD
                                                                                                                                                              95US-0388653.
93US-0017931.
93US-0092977.
94US-0179748.
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                                                                                                                             95US-0478386
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94US-0292597
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                                                                                                                                                                                                                                                                                                                (HARD ) HARVARD COLLEGE.
(STRD ) UNIV LELAND S ST
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-609192/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV62953.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Influenza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-1998;
                                                                                                                                                                                                                                        11-FEB-1994;
18-AUG-1994;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9840394-A1
                                                                                                                                                                                                                                                                                                                                                                                        Wandless TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-1998
                                                                                                                           07-JUN-1995;
                                                                                                                                                                14-FEB-1995;
                                                    US5830462-A
                                                                                         03-NOV-1998
                                                                                                                                                                                   12-FEB-1993
                                                                                                                                                                                                     16-JUL-1993
                                                                                                                                                                                                                          07-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                       Belshaw P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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AAW66198

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Gaps

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The present sequence represents the 12CA5 epitope of haemagglutinin. It is recognised by the polyclonal rabbit antibody HA.11. The sequence was produced by annealing 2 primers encoding the present sequence. These were used to create a epitope tag at the end of human betal-adrenergic receptor (betal-AR) cDNA, which is used to create the transgene of the invention. The specification describes a transgenic animal, especially a mouse, which has incorporated into its genome a transgene comprising a heart tissue-specific promoter operatively linked to a coding sequence comprising betal-AR, the transgene being expressed in at least the myocardium of the heart of the transgenic animal. The transgenic animal can be used as a model for heart muscle disease and heart failure in a mammal. The transgene can also be used for treating heart failure.
Transgenic mice as models for heart disease - having incorporated in their genome a heart tissue-specific promoter operatively linked to DNA coding for a beta-1-adrenergic receptor
                                                                                                                  Example 1; Page 15; 40pp; English.
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1 YPYDVPDYA 9 ||||||||||||| 1 ypydvpdya 9 QQ δ

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Gaps

0;

100.0%; Score 55; DB 19; Length 9; 100.0%; Pred. No. 4.3e+05; Live 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 9; Conservative

Seguence

Search completed: April 11, 2002, 10:15:43 Job time: 93 sec

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Gaps
Sequence Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCURMATION:
APPLICANT: ROGET BEENT
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RETHODS
TITLE OF INVENTION: MOLECULES AND METHODS
CORRESPONDENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STREET: 225 Franklin Street
CITY: Boston
STREET: 3.5" Diskette, 1.44 Mb
CONUTRY: U.S.A.
ZIP: MASSACHUSETTE
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.1)
CONFRYING SYSTEM: MS-DOS (Version 5.1)
CORRENT APPLICATION NUMBER: US/08/011,398B
FILING DATE: 29 JAN 1993
CLASSIFICATION NUMBER: US/08/011,398B
FILING DATE: 29 JAN 1993
CLASSIFICATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 617) 542-5070
TELLEPHONE: (617) 542-5070
TELLEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 55; DB 1; Length 9; larity 100.0%; Pred. No. 1.6e+05; Conservative 0; Mismatches 0; Indels
                 US-08-968-747-12
US-09-156-85-19
US-09-130-133-16
US-09-136-613-36
US-09-158-010-19
US-09-158-010-19
US-09-168-010-19
US-09-108-09-17
US-09-108-966-17
US-09-108-966-17
US-09-108-966-17
US-09-108-966-17
US-09-182-950-8
US-09-182-950-8
US-09-451-905-36
US-09-451-905-36
US-09-451-905-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08011398B; Patent No. 5512473
GENERAL INFORMATION:
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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Matches 9; Conserv
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-011-398B-6
  Query Match
  APP11
                                                                                                                                                                                             (without alignments)
8.190 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, A Sequence 6, A Sequence 19, Sequence 19, Sequence 10, Sequence 119, Sequence 117, Sequence 117, Sequence 11, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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Sequence 1
Sequence 1
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Sequence 2
Sequence 2
                                                                                                                                                                 April 11, 2002, 10:14:10 ; Search time 24.73 Seconds
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. /cgn2_6/ptodata/2/laa/5A_COMB.pep: *

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. /cgn2_6/ptodata/2/laa/6A_COMB.pep: *

. /cgn2_6/ptodata/2/laa/BB_COMB.pep: *

. /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep: *

. /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep: *

. /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep: *
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-090-148-2
US-08-177-925-6
US-08-634-060-31
US-08-646-051-6
US-08-464-051-6
US-08-477-837-28
US-08-477-837-28
US-08-478-366-19
US-08-478-366-19
US-08-695-19
US-08-690-011A-17
US-08-690-011A-49
US-08-695-65-4
US-08-685-559-14
US-08-687-559-14
US-08-687-559-14
US-08-687-559-14
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5-08-483-898-19
5-09-087-716-19
5-08-853-7338-28
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US-08-518-835-6
US-09-157-753-19
US-09-157-230-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                      212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                     US-09-284-787-1
55
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Match Length
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Perfect score:
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                                                                                                                     OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
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APPLICANT: Stockley, Peter George
TITLE OF INVENTION: CAPSID FORMING AND CYSTEINE
TITLE OF INVENTION: MODIFIED CHIMAERIC MS-2-COAT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 55; DB 1; L
100.0%; Pred No. 1.6e+05;
Mismatches 0;
                                                                                                                                                                        CALT: OZID-2804

CAMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 553X
CORDUTER: IBM PS/2 Model 502 or 553X
COPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,225
FILING DATE: 0/30/92
APPLICATION DATA:
APPLICATION NUMBER: 07/969,038
FILING DATE: 10/30/92
ATONEX/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
RECISTRATION NUMBER: 30,162
RECISTRATION NUMBER: 30,162
RECISTRATION NUMBER: 30,162
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONNTRY: U.S.A.
ZIP: 10022-4834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5", 1.44Mb
COMPUTER: IBM Pentium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,982
FILING DATE: 01/03/95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08167982 Patent No. 5698424 GENERAL INFORMATION:
                         E: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Graham & James
STREET: 885 Third Avenue
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                       STATE: Massachusetts
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                              COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YPYDVPDYA 9
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                                               STREET: 225 F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY:
US-08-370-225-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-167-982-1
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APPLICANT: Gyuris, Jeno
APPLICANT: Gyuris, Jeno
APPLICANT: Golemis, Erica
TITLE OF INVENTION: Interaction Trap System for Isolating
TITLE OF INVENTION: No. 5580736el Proteins
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
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                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Mastico, Robert Allan
APPLICANT: Stockley, Peter George
APPLICANT: Talbot, Simon John
TITLE OF INVENTION: Antigen-Presenting Capsid with
TITLE OF INVENTION: Fusion MS2-Coat Protein
NUMBER OF SECUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rosenman & Colin
STREET: STS Madison Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 55; DB 1; I
100.0%; Pred. No. 1.6e+05;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: NY
COUNTRY: U.S.A.
ZIP: 10022-2585
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5", 1.44Mb
COMPUTER: IBM PS2-486
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,148
FILING DATE: 08/11/93
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9101550.3
FILING DATE: 01/24/91
APPLICATION NUMBER: PCT/GB92/00124
FILING DATE: 01/22/92
ATTORNEY AGGNT INFORMATION:
                                                                                                                                                                                   Sequence 2, Application US/08090148
Patent No. 5534257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08370225
Patent No. 5580736
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: NISSENDAUM, ISTAEL
REGISTRATION NUMBER: 27,582
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 940-8636
TELEFAX: (212) 940-6404
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMINO ACID
                            1 YPYDVPDYA 9
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1 YPYDVPDYA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: NOT; MOLECULE TYPE: US-08-090-148-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-08-370-225-6
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Gaps

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                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08464051
Patent No. 5780262
GENERAL INFORMATION:
APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: ABBRESS:
STREET: 225 Franklin Street
                                                                                                                     100.0%; Score 55; DB 1; Length 9; 100.0%; Pred. No. 1.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9;
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100.0%; Pred. No. 1.6e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5° Diskette, 1.44 Mb
MEDIUM TYPE: 3.5° Diskette, 1.44 Mb
COMPUTER: TBW PS/Z Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,051
FILING DATE: 05 JUN 1995
CLASSIFICATION: A35
PRICRATION NUMBER: 08/011,398
FILING DATE: 29 JAN 1993
ATTORNEY AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 00786/160002
TELECOMMUNICATION INFORMATION:
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; Patent No. 5786169
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 542-5070
TELEFAX: (677) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
                                 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; STRANDEDNESS: N/A; TOPOLOGY: linear US-08-464-051-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                    ; MOLECULE TYPE:
US-08-634-060-31
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Patent No. 5712136

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Worksdi, Imre
APPLICANT: Roelvink, Petrus W.

APPLICANT: Roelvink, Petrus W.

TITLE OF INVENTION: THE ADENOVIRAL WEDIATED CELL TARGETING COMMANDED BY

TITLE OF INVENTION: THE ADENOVIRAL PENTON BASE PROTEIN

NUMBER OF SEQUENCES:
ADDRESSEE: Leydig, Voit 6 Mayer, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 55; DB 1; Length 9; 100.0%; Pred. No. 1.6e+05;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Leydig, Voit 6 Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: 111nois
COUNTRY: USA
ZIP: 60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
APPLICATION NUMBER: UK 91140us.c.
FILING DATE: 06/28/91
APPLICATION NUMBER: PCT/GB92/01159
FILING DATE: 06/26/92
ATTORNEY/AGENT INPORMATION:
NAME: Reingold, Jesse
REGISTRATION NUMBER: 20,461
REFERENCE/POCKET NUMBER: Mastico
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 648-1032
TELEPHONE: (212) 648-2449
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 AMINO ACIDS
TELEGRAPHONE: AMINO ACIDS
TELEGRAPHONE: AMINO ACIDS
TENGTH: 9 AMINO ACIDS
TENGTH: 9 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08,303,162
FILING DATE: 08.5EP-1994
CLASSIFICATION: 514
ATIORNEY/AGENT INFORMATION:
NAME: K11yk, John Jr.
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71602
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERIFICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                    AMINO ACID
GY: NOT RELEVANT
TYPE: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YPYDVPDYA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YPYDVPDYA 9
                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-634-060-31
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100.0%; Score 55; DB 1; Length 9; 100.0%; Pred. No. 1.6e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Crabtree, Gerald R.
APPLICANT: Schreiber, Stuart L.
APPLICANT: Spencer, David M.
APPLICANT: Spencer, David M.
APPLICANT: Belshaw, Peter
TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,837
FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/OOCKET NUMBER: 36630-1US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: ARIAD Pharmaceuticals, Inc. STREET: 26 Landsdowne Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, ver.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,386A
FILING DATE: 07/JUN/1995
CLASSIFFCATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Figg. E. Anthony
REGISTRATION NUMBER: 27,195
REFERENCE/DOCKET NUMBER: 27,195
TELECOMMUNICATION INFORMATION:
                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-08-478-386A-19
; Sequence 19, Application US/08478386A
; Patent No. 5830462
; Patent No. 5830462
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WIDTUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC/DOS/MS/DOS
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TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 26 Lands
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YPYDVPDYA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YPYDVPDYA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Namin, Marcel E.
APPLICANT: Hall, Frederick L.
APPLICANT: Tuan, Tal-Lan
APPLICANT: Tuan, Tal-Lan
APPLICANT: Wu, Lingtao
APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transforming Growth Factor B Fusion
TITLE OF INVENTION: Their Use in Wound Healing
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
                   APPLICANT: Gyuris, Jeno
APPLICANT: Golemis, Erica
TITLE OF INVENTION: Interaction Trap System for Isolating
TITLE OF INVENTION: No. 5786169el Proteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 55; DB 1; 100.0%; Pred. No. 1.6e+05;
                                                                                                                                                                                                                                             COUNTY: U.S.A.

ZIP: 0110-2804

COUNTYER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: IBM PS/2 Model 502 or 555X

OPPRATING SYSTEM: MS-DOG (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,859

FILING DATE: January 9, 1995

PROINTARTON NUMBER: 08/370,225

FILING APPLICATION DATA:

APPLICATION NUMBER: 07/969,038

FILING APPLICATION NUMBER: 07/969,038

FILING DATE: October 30, 1992

ATONEY/AGENT INFORMATION:

NAME: LECh, Karen F.

REGISTRATION NUMBER: 35,238

REGISTRATION NUMBER: 35,238

RESIEVENCE/SDOCKET NUMBER: 35,238

RESIEVENCE/SDOCKET NUMBER: 35,238

RESIEVENCE/SDOCKET NUMBER: 35,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Patent No. 5800811

GENERAL INFORMATION:
APPLICANT: Nimni, Marcel E.
APPLICANT: Hall, Frederick L.
APPLICANT: Tuan, Tal Lan
APPLICANT: Wu, Lington
APPLICANT: Cheung, David T.
                                                                                                                                                        ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (617) 542-5070
(617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
Brent, Roger
                                                                                                                                                                                                                                 Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Los Angeles
California
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                                                                                                                                                                                                         Boston
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US-08-461-859-6
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                                                                                                                                                                                                           CITY: B
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
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GENERAL INFORMATION:
APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                           Sequence 6, Application US/08462498
Patent No. 5852169
GENERAL INFORMATION:
APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
SCHEEDPONDENCE ADDRESS:
ADDRESSE: ALSH & ALCHARDS
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 55; DB 2; Length 9; 100.0%; Pred. No. 1.6e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SUFFWARE: WOTDERfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA;
APPLICATION NUMBER: 08/011,398
FILING DATE: 29 JAN 1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
RECISTATION NUMBER: 30,162
RECISTATION NUMBER: 00786/160001
TELECOMMUNICATION INFORMATION:
TELEPAN: (617) 542-5070
TELEFAX: (617) 542-5070
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 60, Application US/08922267A ; Patent No. 5861239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                  Massachusetts
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                                                                                                                                                                                                                                                                                                            CITY: Boston
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                                                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                      Query Match

100.0%; Score 55; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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WEDDUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC/DOS/MS/DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/292,597
FILING DATE: 18/AUG/1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Gerald R. Crabtree
APPLICANT: Schreiber, Stuart L.
APPLICANT: Spencer, David M.
APPLICANT: Wandless, Thomas J.
APPLICANT: Wandless, Thomas J.
APPLICANT: Belshaw, Peter
TITLE OF INVENTION: Regulated Apoptosis
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIAD Pharmaceuticals, Inc.
STREET: 26 Landsdowne Street
CITY: Cambridge
CITY: Cambridge
CITY: Cambridge
COUNTRY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/08292597 Patent No. 5834266
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: F199, E. Anthony
REGISTATION NUMBER: 27,195
REFERENCE/DOCKET NUMBER: 2054-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 783-6040
TELERAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
SEQUENCE CHARACTERISTICS
LENGTH: 9 amino acids
TYPE: amino acid
                                                                                         / MOLECULE TYPE: protein US-08-478-386A-19
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                                                                             linear
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                                                                     TOPOLOGY:
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APPLICANT: Crabtree, Gerald R.
APPLICANT: Schreiber, Stuart L.
APPLICANT: Spencer, David M.
APPLICANT: Wandless, Thomas J.
APPLICANT: Wandless, Thomas J.
APPLICANT: Ho, Steffan
TITLE OF INVENTION: Regulated Transcription of Targeted Genes and TITLE OF INVENTION: Other Biological Events
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Camphell:
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STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 55; DB 2; I; Pred. No. 1.6e+05;
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APPLICATION NUMBER: US 08/179,748
FILING DATE: US -07-JOH-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFENCE/DOCKET NUMBER: 9-SU 9863
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/08473985 Patent No. 5871753
                               ATTORNEY/AGENT INFORMATION:
NAME: Figg, E. Anthony
REGISTRATION NUMBER: 27,195
REFRENCE/DOCKET NUMBER: 2054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
INFORMATION FOR SEG ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                        E. Anthony
27,195
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
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illarity 100.0%;
Conservative (
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 19
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                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-388-653-19
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Best Local Similarity
Matches 9; Conservai
                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
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CLASSIFICATION:
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US-08-473-985-19
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APPLICANT: Schreiber, Stuart L.
APPLICANT: Spencer, David M.
APPLICANT: Bencer, David M.
APPLICANT: Belshaw, Peter
TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIAD Pharmaceuticals, Inc.
STREET: 26 Landsdowne Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9;
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SOFTWARE: PC/DOS/MS/DOS
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/388,653
FILING DATE: 14-FEB-1995
CLASSIFICATION: 514
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 55; 100.0%; Pred. No.
                                                                                                               CURRENT AND CONTRACT 
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Patent No. 5869337
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 60:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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LENGTH: 9 amino acids
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Best Local Similarity 100.
Matches 9; Conservative
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1 YPYDVPDYA 9
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19-Sequence 17, Application US/08690011A
19-Sequence 17, Application US/08690011A
19-Berth No. 294433
19-Sequence 17, Application US/08690011A
19-Sequence 17, Application US/08690011A
19-Septicawn: VIRSON, Charles R.
19-Sequence 17-Septicawn: VIRSON, Charles R.
19-Sequence 18-Septicawn: VIRSON, Charles R.
19-Sequence 18-Septicawn: VIRSON, Charles R.
19-Septicawn: VIRSON, VIRSON, VIRSON, Charles R.
19-Septicawn: VIRSON, VIRSON, VIRSON, Charles R.
19-Septicawn: VIRSON, VIRSON, VIRSON, VIRSON, Charles R.
19-Septicawn: VIRSON, VIRS
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Query Match 100.0%; Score 55; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels
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MOLECULE TYPE: peptide
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US-08-690-011A-17
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Search completed: April 11, 2002, 10:14:43 Job time: 33 sec THIS PAGE BLANK (USPTG)

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98 YPYDVPDYA 106
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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J02375
J02378
S52173
S52174
S52176
S52176
S52178
S52180
S5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                          US-09-284-787-1
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Perfect score:
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No.
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hemagglutinin prechemagglutinin prechemagglutini	WENTS  SN1289)  J.N.; Regnery, H.L.; Cox, N.J.  NI and H3N2) haemagglutinin sequences obtain	ore 55; DB 2; Length 330; ed. No. 0.022; Mismatches 0; Indels 0; Gaps 0;	SN1389 and IN0190) 1-Jul-1994 #text_change 07-May-1999 . J.R.; Regnery, H.L.; Cox, N.J. INI and H3N2) haemagglutinin sequences obtain	ore 55; DB 2; Length 330; ed. No. 0.022; Mismatches 0; Indels 0; Gaps 0;
30 55 100.0 550 1 HMIV98 31 55 100.0 550 1 HMIV15 32 55 100.0 550 2 JUL15 33 55 100.0 550 2 JUL153 34 55 100.0 550 2 JUL154 35 55 100.0 550 2 JUL155 36 55 100.0 550 2 JUL155 38 55 100.0 550 1 HMIVE2 39 55 100.0 565 1 HMIVE2 40 55 100.0 566 1 HMIVHA 41 55 100.0 566 1 HMIVHA 42 55 100.0 566 1 HMIVHA 43 55 100.0 566 1 HMIVHA 44 55 100.0 566 1 HMIVHA 45 55 100.0 566 1 HMIVHA 46 55 100.0 566 1 HMIVHA 47 55 100.0 566 1 HMIVHA 48 55 100.0 566 1 HMIVHA 49 55 100.0 566 1 HMIVHA 40 55 100.0 566 1 HMIVHA 41 55 100.0 566 1 HMIVE	RESULT JO2374 hemagglutinin - influenza A virus (strain SN1289) C; Species: influenza A virus (strain SN1289) C; Species: influenza A virus C; Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 C; Accession: J02374 R; Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Rei J. Gen. Virol. 74, 2513-2518, 1993 A; Title: Comparison of 10 influenza A (HINI and H3) A; Reference number: J02369; MUID:94065682 A; Residues: 1-330 < ROC A; Residues: 1-330 < ROC A; Experimental source: subtype H3N2 C; Superfamily: influenza virus hemagglutinin	Query Match Best Local Similarity 100.0%; Score 5 Matches 9; Conservative 0; Misma Qy 1 YPYDVPDYA 9	RESULT 2 JQ2375 hemagglutinin - influenza A virus (strain SN C; Species: influenza A virus C; Species: influenza A virus C; Species: influenza A virus C; Accession: J01-1994 # sequence_revision 14-Ju C; Accession: J02375; J02276 R; Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J. J. Gen. Virol. 74, 2513-2518, 1993 A; Title: Comparison of 10 influenza A (HINI A; Reference number: J02375 A; Accession: J02375 A; Accession: J02375 A; Residues: 1-330 cROC> A; Cross-references: GB:L20119 A; Experimental source: subtype H3N2 C; Superfamily: influenza virus hemagglutinin	Ouery Match 100.0%; Score Best Local Similarity 100.0%; Pred. Matches 9; Conservative 0; Mism Oy 1 YPYDVPDYA 9

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A; Molecule type: mRNA
A; Residues: 1-74, Nv, 76-120, Tr, 122-156, Lr, 158-173, Fr, 175-188, Sr, 190-200, Kr, 202-2
A; Residues: EMBL: Z46413; NID: 9609059; PIDN: CAA86548.1; PID: 9609060
A; Experimental source: isolate A/Scotland/142/93
C; Superfamily: influenza virus hemagglutinin
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C.Species: influenza A virus
A.Variety: isolate A/Beijing/333/89
A.Variety: isolate A/Beijing/333/89
C.Species: 07-May-1995 #Sequence_revision 23-Feb-1996 #text_change 20-Sep-1999
C.Species: 07-May-1995 #Sequence_revision 23-Feb-1996 #text_change 20-Sep-1999
B.Ellis, J.S.
R.Ellis, J.S.
A.Description: Antigenic and genetic variation in the haemagglutinin of recently circ A;Reference number: S52173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-74,'N',76-120,'T',122-156,'L',158-173,'F',175-188,'S',190-200,'K',202-2
A; Cross-references: EMBL::46402; NID:g609041; PIDN:CAA86537.1; PID:g609042
A; Experimental source: isolate A/England/471/93
                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-134, K', 136-156, L', 158-173, F', 175-188, S', 190-218, F', 220-225, L', 227
A; Cross-references: EMBL: 246395; NID: 9609027; PIDN: CAA86530.1; PID: 91228087
A; Experimental source: isolate A/England/269/93
A; Accession: S52181
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-134, K', 136-156, L', 158-173, 'F', 175-188, 'S', 190-218, 'F', 220-225, 'L', 227
A; Cross-references: EMBL: 46399; NID: 9609035; PIDN: CAA86534.1; PID: 9609036
A; Experimental source: isolate A/England/328/93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-134, K', 136-156, L', 158-173, F', 175-188, S', 190-218, F', 220-225, L', 227
A; Cross-references: EMBL: 246414; NID: 9609061; PION: CAA86549.1; PID: 9609062
A; Experimental source: isolate A/Scotland/160/93
A; Accession: S52196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. Residues: 1-134, 'K', 136-156,'L',158-173,'F',175-188,'S',190-218,'F',220-225,'L',227 A; Cross-references: EMBL:246415; NID:9609065; PIDN:CAA86550.1; PID:9609066 A; Experimental source: isolate A/Scotland/174/93
                    A;Cross-references: EMBL:246410; NID:9609053; PIDN:CAA86545.1; PID:9609054
A;Experimental source: isolate A/Hong Kong/23/92
A;Accession: S52192
                                                                                                                                                                                       A;Cross-references: EMBL:246409; NID:g609057; PIDN:CAA86544.1; PID:g609058
A;Experimental source: isolate A/Hong Kong/34/90
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A; Residues: 1-347 <ELL.>
A; Residues: 1-677 <ELL.>
A; Cross-references: EMBL:246391; NID:g609022; PI
A; Experimental source: isolate A/Beijing/353/89
C; Superfamily: influenza virus hemagglutinin
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Best Local Similarity
2, Conserve
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                        A; Residues: 1-347 <EL3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-347 <EL2>
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C;Species; influenza A virus
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession: S52173; S52190; S52192; S52181; S52194; S52196; S52184; S52193
R;Ellis, J.S.
R;Ellis, J.S.
Bubmitted to the EMBL Data Library, October 1994
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circula A;Reference number: S52173
A;Accession: S52173
                                                                                                                                                                                                                                                    R;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J. J. Gen. Virol. 74, 2513-2518, 1993
A;Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained A;Reference number: JQ2369; MUID:94065682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: influenza A virus
C;Species: influenza A virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: J02378
R;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J Gen. Virol. 74, 2513-2518, 1993
A;Title: Comparison of 10 influenza A (HIN1 and H3N2) haemagglutinin sequences obtained A;Reference number: J02369; MUID:94065682
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C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: JQ2377
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A;Residues: 1-347 <ELL>
A;Cross-references: EMBL:Z46392; NID:g609020; PIDN:CAA86527.1; PID:g609021
A;Experimental source: isolate A/Beijing/32/92
A;Accession: S52190
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100.0%; Pred. No. 0.022;
Vienatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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100.0%; Pred. No. 0.022;
iive 0; Mismatches 0;
                                                                                                                             - influenza A virus (strain SD0191)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:L20105
A;Experimental source: subtype H3N2
C;Superfamily: influenza virus hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L20102
A;Experimental source: subtype H3N2
C;Superfamily: influenza virus hemagglutinin
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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A; Residues: 1-331 <ROC>
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A; Residues: 1-331 <ROC>
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                                                                                                                             hemagglutinin
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A;variety: isolate A/England/289/93
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession: 552180
R;Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: influenza A virus
A;Varitety: isolate A/England/286/93
C.Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession: S52179
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A:Experimental source: isolate A/England/289/93
C:Superfamily: influenza virus hemagglutinin
                                                                     PIDN:CAA86531.1; PID:g609030
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S52179
hemagglutinin - influenza A virus (isolate A/England/286/93) (fragment)
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hemagglutinin – influenza A virus (isolate A/England/289/93) (fragment)
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11arity 100.0%; Pred. No. 0.023;
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A,Molecule type: mRNA
A;Residues: 1-347 <ELL.
A;Cross-references: EMBL:Z46396; NID:g609029; P1
A;Cross-references: EMBL:Z46396; NID:g609029; P1
A;Experimental source: isolate A/England/284/93
C;Superfamily: influenza virus hemagglutinin
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A;Experimental source: isolate A/England/286/93
C;Superfamily: influenza virus hemagglutinin
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A; Residues: 1-347 <ELL>
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A; Residues: 1-347 <ELL>
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A:Variety: isolate A/England/247/93.
C. Accession: 55216
C. Accession: 55216
C. Accession: 55216
A:RElis, J.S.
Submitted to the EMBL Data Library, October 1994
A:Reference number: 552173
A:Reference number: 552173
A:Reference number: 552176
A:Residues: 1-347 < EMBL.
A:Resid
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C; Species: influenza A virus
A; Variety; isolate A/England/284/93
C; Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C; Accession: 552178
R; Ellis, J.S.
Submitted to the EMBL Data Library, October 1994
A; Description: Antigenic and genetic variation in the haemagglutinin of recently circula A; Reference number: 552173
A; Reference number: 552173
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Avariety: isolate A/England/1/93
Avariety: isolate A/England/1/93
Avariety: isolate A/England/1/93
C; Accession: S52175
B; Ellis, J. S.
B; Ellis, J. S.
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Pred. No. 0.023;
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                C;Species: influenza A virus
A;Variety: isolate A/England/328/93
A;Variety: isolate A/England/328/93
A;Variety: isolate A/England/328/93
C;Date: O'rMay-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession: S52182
B;Ellis, J.S.
B;Ellis, J.S.
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circula A;Reference number: S52173
A;Accession: S52182
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C;Species: influenza A virus
C;Species: influenza A virus
A;Varlety: isolate A/England/347/93
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession: S52183
B;Ellis, J:S
Submitted to the EMBL Data Library, October 1994
A;Reference number: S52173
A;Accession: S52183
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R; Ellis, J.S.
Rsblis, J.S.
Submitted to the EMBL Data Library, October 1994
A; Description: Antigenic and genetic variation in the haemagglutinin of recently circula A; Reference number: $52173
A; Accession: $52185
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C;Species: influenza A virus
A;Variety: isolate A/England/67/94
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
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A; Residues: 1-347 <ELL>
A; Cross-references: EMBL: 246401; NID: 9609039; PIDN: CAA86536.1; PID: 9609040
A; Experimental source: isolate A/England/347/93
C; Superfamily: influenza virus hemagglutinin
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A;Residues: 1.347 <ELL.
A;Cross-references: EMBL:Z46403; NID:g609043; PIDN:CAA86538.1; PID:g609044
A;Experimental source: isolate A/England/67/94
C;Superfamily: influenza virus hemagglutinin
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- influenza A virus (isolate A/England/328/93) (fragment)
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100.0%; Score 55; DB 2; Length 347;

Best Local Similarity 100.0%; Pred. No. 0.023;

Matches 9; Conservative 0; Mismatches 0; Indels
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A; Residues: 1-347 <ELL>
A; Cross-references: EMBL:246400; NID:g609037; PI
A; Experimental source: isolate A/England/346/93
C; Superfamily: influenza virus hemagglutinin
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Ayariety: influenza A virus (isolate A/England/68/94) (fragment)
C;Species: influenza A virus
C;Species: influenza A virus
C;Species: influenza A virus
C;Species: or-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession: 552186
C;Accession: 552186
C;Accession: S52186
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100.0%; Score 55; DB 2; 100.0%; Pred. No. 0.023;
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SEQUENCE FOON N. Stepel J.J., Waterfield M.;

REDILINE=8103085; PubMed=7421990;

REDILINE REPUBMED BY ALVERS, PubMed BY THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.

REDILINE RECEPTORS AND FOR INITIATING INFECTION.

RESPONDED BY A DISULFIDE BOND.

RESP. MO451; HMIVH.

PIR: A04051; HMIVH.

RESP. P03437; A93233.

RESP. P03437; A93233.

RESP. P03437; FHMG.

RESP. P03437; PHMG.

RESP. P03437; PMG.

RESP. P03437; PHMG.

RESP. P03437; PMG.

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21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN)
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llarity 100.0%; Pred. No. 0.01;
Conservative 0; Mismatches 0; Indels
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
NCBL_TaxID=11489;
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                                                                                                                                                                                               SEQUENCE FROM N.A. MEDAMED-6164798; Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.; Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.; Mattigenic drift in the hemagglutinin of the Hong Kong influenza subtype: correlation of amino acid changes with alterations in viral
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                             13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ (CONTAINS: HEMAGGLUTININ HAI CHAIN) (FRAGMENT).
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13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ (CONTAINS: HEMAGGLUTININ HAI CHAIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 55; DB 1; Length 328; 100.0%; Pred. No. 0.013;
                                                                                          Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Influenza virus A and B group; Influenza A viruses;
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                                                                                 Influenza A virus (strain A/England/878/69).
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                        Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.;
"Antigenic drift in the hemagglutinin of the Hong Kong influenza subtype: correlation of amino acid changes with alterations in viral antigenicity.";
J. Virol. 37:845-853(1981).
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
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Both G.W., Sleigh M.J.;
"Conservation and variation in the hemagglutinins of Hong Kong
subtype influenza viruses during antigenic drift.";
J. Virol. 39:663-672(1981).
-:- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P03441; 083961; 083962; 21-JUL-1986 (Rel. 01, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 20-AUG-2001 (Rel. 32, Last annotation update) HEMAGGLUTININ HAZ CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Envelope protein; Hemagglutinin; Glycoprotein
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                     MEDLINE-81194918; PubMed-6164798;
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Pfam; PF00509; Hemagglutinin; 1.
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SEQUENCE FROM N.A.
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HEMA_IADH2
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                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
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-1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HAZ) LINKED BY A DISULFIDE BOND.
           SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
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Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
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                                   SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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12582, 084021; 084022;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1989 (Rel. 40, Last annoration update)
HEMAGGLUTININ PRECURSOR [CONTALINS: HEMAGGLUTININ HAI CHAIN;
                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Influenza A virus (strain A/Duck/Hokkaido/5/77).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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FBD2EC200689CBE5 CRC64;
RECEPTORS AND FOR INITIATING INFECTION.
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HEMAGGLUTININ HAZ
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ProDom; PD00225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
CHAIN 1 328
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Best Local Similarity
Matches 9; Conserv
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SUBUNT: HOMOTRIBER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LIRKED BY A DISCULEIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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HEMAGGLUTININ HA2 CHAIN.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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MEDILINE-87265458; Pubmed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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12583; 084011;
01-0CT-1989 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 140, Last annoctation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.023;
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                       InterPro; HMIV77.
InterPro; IPR001364; Hemagglutn.
Probom; PR00509; Hemagglutinin; 1.
Probom; PD000225; Hemagglutin; 1.
NoN_TER I Hemagglutinin; Glycoprotein.
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InterPro: IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutini; l.
ProDom; PD000225; Hemagglutn; l.
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                                                                                                                                                          EMBL; M16737; AAA43143.1; -.
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Best Local Similarity
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NCBI_TaxID=11358;
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N-LINKED (GLCNAC. . .) (POTENTIAL) 6C30BF67CFDCB7DE CRC64;

61577 MW;

550 AA;

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-1- SUBUNIT: HOMOTRINER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISSULFIDE BOND.
-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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                                                                        N-LINKED (GLCNAC. .) (POTENTIAL).
X -> N (IN PIR DATA BAN).
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Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
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| 19.1584, 084012; 089793; | 01-0CT-1999 (Rel. 12, Created) |
| 10.1-0CT-1999 (Rel. 12, Last sequence update) |
| 10.1-0CT-1999 (Rel. 12, Last sequence update) |
| 10.1-0CT-1999 (Rel. 40, Last annotation update) |
| 10.1-0CT-1999 (Rel. 
                                                                                                                                                                                                                                                                    100.0%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.023;
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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HEMAGGLUTININ HAZ
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PIR; C27813; HMIV33.
InterPro; IPR001364; Hemagglutn.
Probom; PE00509; Hemagglutnin; 1.
Probom; PD000225; Hemagglutnin; 1.
Envelope protein; Hemagglutnin; Glycoprotein.
I 1 328 HEMAGGLUTININ HA1
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-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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-i- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS CELL RECEPTORS AND FOR INITIATING INFECTION.
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HEMAGGLUTININ HAZ CHAIN.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
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                                                                                                                                                                                                                                                                   | HEMA_IADH4 | STANDARD; | PRT; | 550 AA. |
| 191268: 084013; 084014; 084014; 01-0CT-1989 (Rel. 12, Created) |
| 01-0CT-1989 (Rel. 12, Last sequence update) |
| 01-0CT-1989 (Rel. 14), Last annotation update) |
| HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
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100.0%; Score 55; DB 1; Length 550. 100.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Influenza A virus (strain A/Duck/Hokkaido/7/82).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                Indels
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A16B2CF8CBBBD9D0 CRC64;
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Envelope protein; Hemagglutinin; Glycoprotein.
NON_TER 1
                                                0; Mismatches
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InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
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                                                  Conservative
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550 AA;
Query Match
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Best Local Similarity
Matches 9; Conserv
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                                                                                                1 YPYDVPDYA 9
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HEMA_IADH4
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RESULT 9 HEMA\_IADH6

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                                                                                                                                                                                                                                                                                      VICOLOGY 159:109-119(1987).

-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.

-!- SUBGNIT: HOWOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.

-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-STA55458, Pubmed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F1-20-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECHSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN;
HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN;
HEMAGGLUTININ HA2 CHAIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Influenza A virus (strain A/Duck/Hong Kong/7/75).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Vifluenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                              Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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                                                                 Influenza A virus (strain A/Duck/Hokkaido/10/85).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00509; Hemagglutinín; 1.
ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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PIR; G27813; HMIV15.
InterPro; IPR001364; Hemagglutn.
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550 AA;
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Matches 9; Conser
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                                                                                                                                               NCBI_TaxID=11363;
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P43257;
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HEMA_IADHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ducks...

4. VICOLOGY 159:109-119(1987).

- I FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INPECTION.

- I SUBUNIT: HOWOTHERNER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISJULEIDE BOND.

- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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HEMAGGLUTININ HAZ CHAIN.
N-LINED (GLCNAC. . .) (POTENTIAL).
Y -> N (IN PIR DATA BANK).

### 678CD85F44736CFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-87265458; Pubmed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                               HEMA_IADH6 STANDARD; PRT; 550 AA.
P12587; Q84017;
01-0CT-1989 (Rel. 12, Created)
01-0RP-1900 (Rel. 14, Last sequence update)
20-ANG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                          Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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                                                                                                                                                                                                                                                                       Influenza A virus (strain A/Duck/Hokkaido/9/85).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00509; Hemagglutini; 1.
Probom; PD000225; Hemagglutini; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
NON_TER 1 1 1
CHAIN 1 728
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Best Local Similarity
98 YPYDVPDYA 106
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                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=11362;
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                                 -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-91341491; PubMed=1875195;
Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;

Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;

A/Hong Kong/68 (H3N2) strain emerged.";
J. Gen. Wirol. 72:2007-2010(1991).

-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.

-I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
           Yasuda J., Shortridge K.F., Shimizu Y., Kida H.; "Molecular evidence for a role of domestic ducks in the introduction
                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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P43258;
01-NOY-1995 (Rel. 32, Created)
01-NOY-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                               HEMAGGLUTININ HA1 CHAIN. HEMAGGLUTININ HA2 CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 55; DB 1;
Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                       Envelope protein; Hemagglutinin; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
MEDLINE-91341491; PubMed-1875195;
                                                                                                                                                                                                                                          EMBL; D00929; BAA00769.1; -.
HSSP; P03437; 5HMG.
InterPro; IPR001364; Hemagglutn.
                                                                                                                                                                                                                                                                              Pfam: PF00509; Hemagglutinin; 1. ProDom; PD000225; Hemagglutn; 1.
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HEMA_IADHL
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N-LINKED (GLCNAC. . . ) (POTENTIAL).
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                        SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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00-NG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECRSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN;
HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD00225; Hemagglutinin; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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AND HA2) LINKED BY A DISULFIDE BOND
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01-NOV-1995 (Rel. 32, Last seq
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88306236; PubMed-3407150; Katz J.M., Webster R.G.; "Antigenic and structural characterization of multiple subpopulations of H3N2 influenca virus from an individual."; Virology 165:446-456(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL RECEPTORS AND FOR INITIATING INFECTION.

-!- SUBUNIT: HOMOTRIBE. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISQUEIDE BOND.

-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
N-LINKED (GLCNAC. . ) (POTENTIAL).
91.9A1E094DA28BACD2 CRC64;
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01-0CT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                              100.0%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.023;
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Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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HSSP; P03437; 2HMG.
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HEMA_IAME6
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MEDLINE-91341491; PubMed-1875195;
Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
"Molecular evidence for a role of domestic ducks in the introduction of avian H3 influenza viruses to pigs in southern China, where the A/Hong Kong/68 (H3NZ) strain emerged.";
J. Gen. Virol. 72:22007-2010(1991).
I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
(FAL AND HAZ) LINKED BY A DISULEIDE BOND.
(HAL AND HAZ) LINKED BY A DISULEIDE BOND.
SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN) (FRAGMENT).
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Probom; P000225; Hemagglutinin; 1.
Probom; P000225; Hemagglutinin; 1.
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NON_TER 1 328 HEMAGGLUTININ HAI
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  or send an email to license@isb-sib.ch).
                                                          InterPro; IPR001364; Hemagglutn. Pfam; PF00509; Hemagglutinin; 1. ProDom; PD000225; Hemagglutn; 1.
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STARIN-TOKYO1537, TOKYO1511;
A MOIT S., Sekine H.; Tokyo1511;
T "HA1 domain of Influenza A (H3N2) virus.";
L Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; A8013807; BAA77285.1; -..
InterPro; IPR001364; Hemagglutin.
P fam; PR000509; Hemagglutin. 1.
R PRINTS; PR00329; HEMAGGLUTN12.
R PRINTS; PR00325; Hemagglutin; 1.
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
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26477 MW; 4566C8E7210FB558 CRC64;
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01-NOV-1999 (TrEMBLrel, 12,
01-NOV-1999 (TrEMBLrel, 12,
01-JUN-2001 (TrEMBLrel, 17,
HEMAGGLUTININ (FRAGMENT).
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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sp_phage:*
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Maximum DB seq length: 200000000
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A SEQUENCE FROM N.A.

A Mori S., Sekine H.;

L Submitted (MAY 1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AB013813; BAA77291.1; ...

R EMBL; AB013819; BAA77287.1; ...

R EMBL; AB013811; BAA77289.1; ...

R EMBL; AB013812; BAA77289.1; ...

R EMBL; AB013812; BAA77290.1; ...

R EMBL; AB013812; Hemagglutn.

R Pfam: PF00509; Hemagglutinin; 1.

R Propom; PD000225; Hemagglutn; 1.
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                                                          Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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STRAIN-72, 70, AND 71;
Nagashima M., Moril S., Sekine H.;
"Influenza A virus gene for hemagjlutinin.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mori S., Sekine H.;
"Hal domain of Influenza A (H3N2) virus.";
"Hal domain of Influenza A (H3N2) virus.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, A8014062; BAA77286.1;
EMBL, A8014060; BAA77292.1;
EMBL; A8014061; BAA77293.1;
                                                                                                                                                                                                                                                                          26493 MW; 457455682C8D28D7 CRC64;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ (FRAGMENT).
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Last annotation update)
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Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
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Matches 9; Conservative
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236 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRIN=A/THWAN/2192/96;
Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
"Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in
                                                                                                                                                                                                                                                                                                                                                                        influenza A virus (A/Taiwan/2034/96(H3N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=95240;
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                  100.0%; Score 55; DB 12; Length 236; 100.0%; Pred. No. 0.05;
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EMBL, AF139937, AAD34854.1; -.
InterPro: IPR001364; Hemagglutn.
Pfam: PPR0039; Hemagglutinn: 1.
PRINTS, PR00329; HEMAGGLUTN12.
ProDom: PD000225; Hemagglutn: 1.
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
EMBL, AF139936; AAD34853.1; -
InterPro; IPR001364; Hemagglutn.
PF00509; Hemagglutinin; 1.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
H3 HEMAGGLUTININ (FRAGMENT).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
H3 HEMAGGLUTININ (FRAGMENT).
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Best Local Similarity 100.
Matches 9; Conservative
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286 AA;
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SEQUENCE FROM N.A.
                                                                                                                      NCBI_TaxID=95241;
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57 YPYDVPDYA 65
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
10-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1 Influenza A virus (A/Finland/583/98(H3N2)).
Viruses; sarNA negative-strand viruses; Orthomyxoviridae;
1 Influenza virus A and B group; Influenza A viruses; Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Acceptable protective efficacy of influenza vaccination in young military conscripts in circumstances of incomplete antigenic and genetic match."; Vaccine 0:0-0(2001).
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STRAIN-A/FINLAND/583/98;
Pyhaia R., Haanpaa M., Kleemola M., Tervahauta R., Visakorpi R.,
Kinnunen L.;
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100.0%; Score 55; DB 12; Length 325;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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100.0%; Pred. No. 0.073;
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InterPro; IPR001364; Hemagglutn.
Pfam; PR00359; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
PRODOM; PD000225; HEMAGGLUTN12.
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EMBL; AF008782; AAB63719.1; -
InterProx; IPR001364; Hemagglutn; -
Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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SEQUENCE FROM N.A.
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STRAIN-ATDAINMAN/2191/96;
Shih S.-R., Chen S.-H., Wu S.-L., HO C.-C.;
"Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        influenza A virus (A/Taiwan/2191/96(H3N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
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STRAIN-A/ILLINOIS/5/95(H3N2);
Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF139932; AAD34849.1; -.
InterPro: IPR001364; Hemagglutn.
Pfan; PF00509; Hemagglutini; 1.
PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
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                                                                                                                                              32059 MW; CB51B092AAD0D7D8 CRC64
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ GENE (FRAGMENT).
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PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
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"Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus isolates circulating in Canada during the 1997/98 Influenza season."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, PR087700; AAC36729.1; ...
InterPro; IPR001364; Hemagglutn.
Probom; PD000225; Hemagglutnin; 1.
Probom; PD000225; Hemagglutn; 1.
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SEQUENCE 327 AA; 36389 MW; 909239953649069E CRC64;
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Osiowy C.K.;
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327 AA;
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Influenza virus A and B group; Influenza A viruses.
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STRAIN-A/PENNSYLVANIA/7/94(H3N2);
STRAIN-A/PENNSYLVANIA/7/94(H3N2);
Straited (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF008188; AAB63725.1;
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutn.i.
ProDom; PD000225; Hemagglutn; 1.
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Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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          Fitch W.M., Bush R.M., Bender C.A., Cox N.J.; Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AF008797; AAB63724.1.; InterPro; IPR001364; Hemagglutn. Pfam; PF00509; Hemagglutnin; 1. ProDom; PD000225; Hemagglutnin; 1. NON_TER
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326 326
326 AA; 36197 MW; 4B84BD4AADC44A77 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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STRAIN=A/NEW_YORK/28/94 (H3N2);
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326 AA;
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EMBL; AF087703; AAC36732.1; - InterPro; IRRO/D184; Hemagglutn.

Pfam; PF00509; Hemagglutin.1; 1.
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Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                Oslowy C.K.;
"Geneflic Characterization of A/Sydney/05/97-like(H3N2) Influenza virus
"Geneflic Characterization of A/Sydney/05/97-like(H3N2) Influenza season.";
submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, *AR087709, AAC36738.1;
InterPro: IPR003364; Hemagglutin.
Probom; PD000225; Hemagglutin.1:
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"Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus
"Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus
"solates circulating in Canada during the 1997/98 Influenza season.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF087701; AAC36730.1;
InterPro; IPR001364; Hemagglutn.
Pfan; PF00509; Hemagglutnin; 1.
ProDom; PD000225; Hemagglutn; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    influenza A virus (A/Sydney/05/97-like(H3N2)).
Virusas; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
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                                                                                                                                 327 AA; 36373 MW; ADBD67D856EBCC96 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ (FRAGMENT).
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                     STRAIN-A/SYDNEY/05/97(H3N2);
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OC Influenza A virus (A/Sydney/05/97-11ke(HNN2)).
OC Viruses; SaRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A viruses.
OX NCBI_TaxID-82372;
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                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                              Listing first 45 summaries
                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                1 YPYDVPDYAGSGSK 14
                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                         US-09-284-787-2
80
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                        Perfect score:
                                                                                                                                                      Scoring table:
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                                                                                                                                  Sequence:
                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                  Database
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0
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                                                                                                              Title:
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Compact Structure
Construct PGGNN-ZE
Exol6 partial prot
Amino acid sequenc
LexA-GAL4 [usion p
HA-tagged I-kappa-Yeast MSH1 protein

Influenza haemagil pSMTN3 fragment fo Peptide encooded b Plasma membrane ta

Thrombopoletin pro Epitope tagged TBP Neural cell adhesi

AAY06273 AAW77291 AAR81355 AAR81356 AAW73369 AAR92254

Expression vector pHOOK-1.GM-CSF fus Anti-Fc gamma rece Anti Fc alpha rece HA tag. Synthetic Thrombopoletin pro GAL4/HA/NUMA fusio HA1 epitope. Infl Mus musculus haema

AAW05097 AAW95558 AAY90725

AAY30054 AAB69626 AAY49751 AAW08425 AAB21192 AAW85003 AAY86206 AAY96709 AAR76070 AAY96145 AAY32764

CSFV envelope prot HM1.24 antigenic p HM1.24 antigenic p HM1.24 antigenic p

AAY32763 AAY32768 AAW17789 AAW44013

AAB30796 AAY49279 AAY49277

Green fluorescent.
Haemagglutinin pep
AMino acid sequenc
Sequence of anglos
Sequence of anglos

ALIGNMENTS

detection; isolation; Human influenza virus haemagglutinin epitope peptide fragment #2. "C-terminal epsilon-bionoyl-amide group" 'note= "N-terminal acetyl group" Haemagglutinin; epitope; monoclonal antibody; fusion protein. Location/Qualifiers AAW59451 standard; peptide; 14 AA (BOEF ) BOEHRINGER MANNHEIM GMBH Hinzpeter M; 96DE-1043314 96DE-1043314 (first entry) Human parainfluenza virus. Grol M, DE19643314-A1 21-OCT-1996; 21-0CT-1996; 23-APR-1998 Emrich T, 

WPI; 1998-241603/22

pTAT-HA linker pol pTAT-HA linker enc Flu-epitope scramb Flu epitope tagged Transdominant effe

AAB07730 AAY20692 AAW27158 AAB29443 AAW21032 AAW49116 AAB45969 AAW48631

21 21 22 12 12 13 13 13 13 13

165 165 165 167 17 17

100.0 93.8 88.8 85.0 83.0 81.2 81.2 81.2 81.2

Chimeric adenovira

Amino acid sequenc Peptide encoded by Peptide E16853Al f Saccharomyces cere

Human influenza vi

AAW59451 AAG63605

us-09-284-787-2.rag

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AAB07730 standard; Peptide; 34
                                                                                                                         07-NOV-2000 (first entry)
                                                                                                     AAB07730;
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                                                           This peptide fragment represents a human influenza virus haemagglutinin eptitope which is used to make monoclonal antibodies with an affinity constant of 108 M-1. Such antibodies are used for detecting and isolating native human influenza virus haemagglutinin (HA), modified HA or HA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a chimeric fusion protein of the invention. The specification describes a chimeric pIX protein having at least one adenoviral pIX domain and a non-native amino acid sequence. The non-native sequence is a ligand that binds to a substrate present on surface cells. The chimeric proteins are used for producing adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                           Gaps
          Monoclonal antibodies to influenza virus haemagglutinin - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric pIX protein useful in an adenovirus gene transfer vector infecting cells comprises at least one adenoviral pIX domain and a
                                                                                                                                                                                                                                                                                                                          Amino acid sequence of N-terminal fusion protein of pIX protein.
                                                                                                                                                                           ;
0
                                                                                                                                                       Length 14;
                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                               pIX protein; chimeric protein; gene transfer vector
                                                                                                                                                     DB 19;
2.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 75; DB 22; L
; Pred. No. 0.00022;
                     detecting and isolating haemagglutinin proteins
                                                                                                                                                     ; Score 80; DB
; Pred. No. 2.7e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wickham TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 26-27; 28pp; English.
                                                                                                                                                                                                                                                                AAG63605 standard; Protein; 165 AA.
                                                                                                                                                    100.0%; S
                                       Claim 7; Page 2; 6pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                      09-FEB-2001; 2001WO-US04233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-FEB-2000; 2000US-0181163.
                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roelvink PW, Kovesdi I,
                                                                                                                                                                         Conservative
                                                                                                                                                                                            1 YPYDVPDYAGSGSK 14
                                                                                                                                                                                                       1 ypydvpdyagsgsk 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene transfer vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-native amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-497066/54.
                                                                                                                                                    Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENV-) GENVEC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 AA;
                                                                                                                       14 AA;
                                                                                                   fusion proteins.
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                                                                                                                                                                                                                                                                                                                                                                            Mastadenovirus
                                                                                                                                                                                                                                                                                                                                                                                                WO200158940-A2
                                                                                                                                                                                                                                                                                                       15-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sednence
                                                                                                                                                                                                                                                                                    AAG63605;
                                                                                                                                                                                                                                                       AAG63605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolation of genetic elements encoding a gene product with a desired activity is carried out in microcapsules where changes in optical activity are detected \dot{\,}
Peptide encoded by amplification product encoding a FLAG-HA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                      Genetic element; optical property; gene product; microcapsule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 71; DB 21; Length 34;
Pred. No. 0.00018;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 12; Page 79-80; 128pp; English.
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ilarity 92.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAA59266
                                                                                                                                                                 WO200040712-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                          Griffiths A,
                                                                                                                                                                                                                                                                                                                               07-JAN-1999;
                                                                                                                                                                                                                        13-JUL-2000
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Best Local Simi
Matches 12;
                                                                                                          Synthetic
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Gaps

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Indels

93.8%; Scort 100.0%; Pred. No. v..

Conservative

Query Match Best Local Similarity Matches 13; Conserv

Length 165;

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(GARD/)

(JUEP/) KRON/) POTT/

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The present sequence is the Saccharomyces cerevisiae alpha mating factor receptor Ste2, which was used in the development of a method to prepare cells presenting on their surface a mutant G-protein coupled receptor (GPCR) binding a desired ligand which the natural receptor cannot. The method comprises generating replicable expression plasmids comprising a coding sequence for a GPCR mutated by one or more amino acids in its transmembrane and/or extracellular domains, and operatively linked expression control sequences, transforming host cells with the plasmids and contacting the cells with the plasmids and contacting the cells with the higand and isolating those which bind. GPCR are natural receptor proteins, i.e. membrane proteins that allow cells presenting mutant GPCR on their surfaces are useful as biosensors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with potential applications in diagnostics and environmental and on-line process monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric protein; fusion protein; FLICE like inhibitor protein; FLIP; Fas; TNF; apoptosis; caspasse-8; ligand; T cell; thymocyte; tumour specific antigen; immune response; therapy, prophylaxis; diagnosis; HIV; human immunodeficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cells for surface expression of mutants of natural G-protein receptor - where the mutants can bind a ligand that the natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.8%; Score 67; DB 18; Length 481; 92.3%; Pred. No. 0.012; 1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Pages 13-15; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor cannot, useful as biosensors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                             (BRBI-) BRITISH BIOTECH PHARM LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB03963 standard; Peptide; 16 AA.
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                                                                                                                                                                                                                                            96GB-0006126
                                                                                                                                                                                           97WO-GB00746
  on-line process monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pTAT-HA linker polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 83.8
Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                            WO9735985-A1
                                                                                                                                                                                           19-MAR-1997;
                                                                                                                                                                                                                                            22-MAR-1996;
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                                                                                                                                             02-OCT-1997
                                                                                                                                                                                                                                                                                                                                              Edwards RM;
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Tether1 and control plasmids.

Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or compounds of the structure or formula signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4); B is a C-terminal inding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34);

R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH P which avoids the need for regular injections to treat osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammallan conditions characterized by decreases in bone mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           compound comprising an amino terminal signaling functional domain
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                                                                  PTH: parathyroid hormone; conjugate; bone mass; bone reformation; PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
                  Peptide E16853A1 for construction of rTether1 containing HA-tag.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68; DB 21; Length 32;
Pred. No. 0.00049;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
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78.6%;
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Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       ) GARDELLA T J.
) KRONENBERG H M.
) POTTS J T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JUEPPNER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 AA;
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                                                                                                                                                                                         WO200039278-A2.
                                                                                                                                                                                                                                                                                        30-DEC-1999;
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                                                                                                                                          Synthetic.
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AAW27158;

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AAW27158 RESULT

Sequence

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Gaps

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Lou Gehring's disease; viral infection; HIV; bacterial infection.
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AAW41032
ID AAW4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-apoptotic polypeptide which inhibits apoptosis of lymphocytes in combination with a transport group is described. The transport group is capable of transport group is described. The transport group is capable of transporting the chimeric group or fusion peptide across the cell membrane. The anti-apoptotic polypeptide is FLICE-like inhibitor protein (FLIP) which inhibits Fas and TWF mediated apoptosis by inhibiting binding of Caspase 8 to the Fas receptor complex, thus shutting off the downstream Fas signalling pathway. The chimeric group and fusion peptide are useful for inhibiting ligand-induced apoptosis by bringing them into contact with T cells. The chimeric group is useful for expanding T cells in vitro e.g. T cells specific for particular antigens such as tumour-specific antigen, for enhancing particular antigens such as tumour-specific antigen, for enhancing particular antigens such as tumour-specific antigen, for enhancing are useful for their apoptosis of chronically activated CD4 transpertic, prophylactic or chimeric group is also useful for therapeutic, prophylactic or diagnosis of intracellular delivery of small molecules and conding such polypeptides. Two primers (AAA54298) were used to amplify the FILP CDNA for subcloning into the Xhol-Nool site of the pHA-TAT vector which contains the N-terminal protein contains the N-terminal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein transduction domain; fusion molecule; therapeutic agent; drug targetting; drug discovery; cell transduction; bioavailability; vaccine; nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; pre-senile dementia; epilepsy; seizure; compulsive behaviour; meningitis; encephalitis; ischaemia; spongiform encephalopathy; dyslexia; age-related memory loss;
                                                                                                                                                                                                                                                                                                                                Fusion polypeptide useful for inhibiting ligand-induced apoptosis, comprises portion of anti-apoptotic polypeptide linked to a transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein. Tat is a preferred transport moiety.
                                                                                                                                            (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB29443 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 9; 89pp; English.
                                                                                                                                                                                                                               Paya C, Algeciras-schminich A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pTAT-HA linker-encoded peptide.
                                                                                                                                                                                        (ALGE/) ALGECIRAS-SCHMINICH A.
                                                                                                   99US-0128021.
                                       05-APR-2000; 2000WO-US09002.
                                                                                  99US-0127867
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                                                                                                                                                                                                                                                                    WPI; 2000-664988/64.
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Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YPYDVPDYAGS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 AA;
                                                                                                                                                                                                                                                                                           N-PSDB; AAA54300
                                                                                05-APR-1999;
                                                                                                   06-APR-1999;
12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB29443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a cardiovascular drug, an antitumour drug, an analgesic, an antinflammatory, a diagnostic marker or a drug for the treatment or prevention of a central or peripheral nervous system disorder. The central nervous system (CNS) disorder is especially Alzheimer's disease, Parkinson's disease, Huntington's disease, and also includes pre-senile dementia, epilepsy and seizures, compulsive behaviour, meningitis (including viral and bacterial meningitis), encephalitis, ischaemia, scrapie (or related spongiform encephalopathies), dyslexia, age-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          resistant microorganisms using a suitable fusion molecule; a mammal comprising a covalently linked fusion molecule; and a mammal adapted for experimental use in which at least one transduction molecule has been transduced into essentially all the cells of the mammal. The fusion molecule is used to deliver a therapeutic agent to a mammal, especially a human. The linked molecule may be a vaccine, an anti-infective drug,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           memory loss or Lou Gehring's disease. Fusion molecules can also be used to Xill Virally infected cells, especially those infected with HIV. The vaccines are used to treat or prevent bacterial or viral infections. The methods are a highly effective means for transducing a molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              size,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel fusion molecule comprising at least one protein transduction domain (PTD) and at least one linked molecule, where the linked molecule has therapeutic or prophylactic activity against a medical condition. The invention also relates to methods of drug discovery in which the test compound is linked to a suitable transducing protein and introduced to a cell; a method of killing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are associated with many therapeutic agents (e.g., large molecular si
hydrophobicity, hydrophilicity, biological resistance), by providing
efficient transduction of the transfer cell. The present sequence
represents a protein transduction domain used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      into an entire mammal or into specific cells, tissues, organs and systems within it. They also overcome bioavailability problems that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion molecules comprising protein transduction domains and therapeutic agents, useful for treating e.g. Alzheimer's and Parkinson's diseases, dementia and epilepsy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.2%; Score 65; DB 21; Length 16; 100.0%; Pred. No. 0.00071; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW41032 standard; Protein; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 2; 191pp; English.
Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                 99US-0122757.
99US-0151291.
                                                                                                                                                                                                                                                                                              28-FEB-2000; 2000WO-US05097.
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNIW ) UNIV WASHINGTON
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                                                                                                                           WO200062067-A1.
                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-1999;
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                                                                                                                                                                                                              19-OCT-2000
                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dowdy SF;
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This peptide comprises a Flu epitope tagged scrambled peptide.

Murine 1071/2 Clone 8 cells were infected with pBabe puro

Extravirus constructs containing a sequence coding for the Flu
scrambled epitope or an inhibitor peptide (see AAW2917) identical

cothe C2 region of protein Kinase C (PKA) isozymes. Control clone

cothe C2 region of protein Kinase C (PKA) isozymes. Control clone

cothe C2 region specimently cytoplasmic and perinuclear staining,

while PMA induced cells showed translocation to the nucleus. Cells

infected with constructs coding for the scrambled peptide showed

similar staining. Those infected with constructs coding for

the C2 region showed predominantly cytoplasmic and perinuclear staining in both control and PMA induced cells. Novel outcomes con

cocur upon expression of peptides in cells. A claimed method of

screening for transdominant intracellular bioactive agents (A) able

cother the phenotype of a cell comprises: (a) introducing a

library of different randomised nucleic acids (I) into cells; and

(B) screening the cells for altered phenotype due to presence of

(A). Also new are: (1) a library of retroviruses containing

containing the library of (1), preferably integrated into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Intracellular transdominant bioactive agent; screening; cell phenotype; effector peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening for transdominant intracellular active agents able to alter cell phenotype - useful for examining for changed phenotype, particularly to identify potential drugs with e. g. antitumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transdominant effector peptide associated screening peptide #49
altered phenotype; retrovirus; library; signal transduction; antitumour; pBABE; influenza virus; flu; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.2%; Score 65; DB 18; Length 1,
100.0%; Pred. No. 0.00076; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 53; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB45969 standard; Peptide; 17 AA.
                                                                                                                                                                                            97WO-US01019
                                                                                                                                                                                                                                       96US-0589911.
96US-0589109.
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nes 11; Conservative
                                                                                                                                                                                                                                                                                                      (RIGE-) RIGEL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-393611/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AA;
                                                                                                          WO9727212-A1
                                                                                                                                                                                            23-JAN-1997;
                                                                                                                                                                                                                                       23-JAN-1996;
23-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-APR-2001
                                                                                                                                                   31-JUL-1997.
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                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB45969;
                                                                                                                                                                                                                                                                                                                                                 Noaln GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a scrambled flu-epitope peptide, and can be used in the method of the invention. The method is for screening for transdominant bloactive agents (A) able to alter the phenotype of a comprises: (a) introducing a library of different randomised nucleic acids (I) into cells; and (b) screening the cells for altered phenotype due to presence of (A). (A) are potential pharmaceuticals, from their effect on signalling pathways. A particular application is to identify peptides, encoded by (I), that have antitumour activity or are able to increase sensitivity to, or reduce toxicity of, known antitumour agents. More generally the method can identify agents for treatment of many other conditions, e.g. cardiovascular diseases, anglogenesis, atherosclerosis, obsestly, neurodegeneration, bone disease, viral and other infections,
                                                                                                                                              Transdominant bloactive agent; phenotype alteration; signalling pathway; antitumour agent; cardiovascular disease; angiogenesis; atherosclerosis; obesity; neurodegeneration; bone disease; infection; allergy; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening for trans-dominant active agents able to alter cell phenotype - useful to identify potential drugs with e. g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transdominant intracellular effector peptide; RNA; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.2%; Score 65; DB 18; L. 100.0%; Pred. No. 0.00076; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flu epitope tagged scrambled peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 53; 91pp; English.
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                                                                                                          Flu-epitope scrambled peptide.
                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US01048.
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96US-0589109
                                                               12-MAY-1998 (first entry)
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noaln GP, Rothenberg SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phenotype - useful to
anti-tumour activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-393612/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        flu-epitope peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 AA;
                                                                                                                                                                                                                                                                                  Influenza virus.
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                                                                                                                                                                                                                                                                                                                           WO9727213-A1
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23-JAN-1996;
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                                                                                                                                                                                                                                                              Synthetic
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                      AAW41032;
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94US-0303162.
                               Roelvink PW,
          (GENV-) GENVEC INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW46332;
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                              This invention describes novel in vitro screening methods (1) for a transdominant intracellular bloactive agent capable of altering the phenotype of a cell. (1) comprises: (a) introducing a molecular library of randomized candidate nucleic acids into several cells; and (b) screening the cells for a cell exhibiting an altered phenotype, where the altered phenotype is due to the presence of a transdominant bioactive agent. The methods are particularly useful for screening intracellular transdominant effector peptides and RNA molecules selected inside living cells from randomized pools. (1) is also useful for introducing random libraries into cells to screen for bloactive compounds. The methods allow lighous and their corresponding expression products in a single step. In addition, the methods allow screening in the absence of significant prior characterization of the cellular defect.
                                                                                                                                                                                   Methods for screening intracellular transdominant effector peptides and RNA molecules comprise delivering random oligonucleotides to cells, which are then screened for an altered phenotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Short-shafted adenoviral fibre; ssAF; penton base; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric adenoviral penton base protein epitope 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                   81.2%; Score 65; DB 22; I
100.0%; Pred. No. 0.00076;
iive 0; Mismatches 0;
                                                                                                                                                                                                                           Example 1; Column 79-80; 57pp; English.
                                                                                                            (STRD ) UNIV LELAND STANFORD JUNIOR. (RIGE-) RIGEL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW48631 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bispecific antibody; HIV; cancer.
                                                           97us-0789333
                                                                               96US-0589108.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                            Rothenberg SM, Nolan GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                               WPI; 2001-060084/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YPYDVPDYAGS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                      17 AA;
Unidentified
                                                            23-JAN-1997;
                                                                               23-JAN-1996;
23-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-AUG-1996;
                   US6153380-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-AUG-1997;
                                      28-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW48631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
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The present peptide sequence is incorporated into an adenoviral fiber.

The fiber protein and its penton base are used by the adenovirus to

The fiber protein and its penton base are used by the adenovirus to

infect a cell. The invention claims for a transfer vector which contains

DNA encoding a short-shafted adenoviral fibre (ssAF). The adenoviral

CC benton base can be modified by incorporating sequences for a ligand to a

CC all surface receptor or sequences that allow binding to a bispecific

antibody. Bispecific antibodies raised against the present peptide

CC antibody one end of the antibody molecule to bind to the fiber and the

CC ther end to bind specifically to a cell surface receptor. Therefore

CC this method enables targeting of the adenovirus to a desired cell-surface

CC this method has end to a non-native amino acid sequence either

CINTO the penton base or the fibre knob. The non-native amino acid

Sequence can be such that it enables direct or indirect binding agent

CC means of a bispecific or multispecific binding agent, of the adenovirus

CC calconius to attach to a cell and therefore effect entry into the cell

Would reduce the level or efficiency of adenoviral penton base binding to

CC the adenovirus to a qiven cell. The transfer vector is claimed

CC the adenovirus to a given cell. The transfer vector is claimed

CC the adenovirus to a given cell. The transfer vector is claimed

CC the buseful for expressing therapeutic genes, for treating inherited

CC beautogenic infections (e.g. HIV infections) and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemagglutinin sequence of a chimeric adenovirus penton base protein.
                                                                                                                                                                                        Short-shafted adenoviral fibre constructs - used for producing products that facilitate entry into target cells, useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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Wickham TJ;
                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 39; 98pp; English.
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                                                                                                                                                                                                                                                                                               therapy of cellular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0634060.
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                                                                                            WPI; 1998-169180/15
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Gaps

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This invention describes a novel method for the selection of monoclonal antibodies (MAb) which comprises (i) fusing B lymphocytes with myeloma entibodie antibody-producing hybridomas such that the antibodies are presented at the surface of the hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murthe lammnoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I k(k) molecule; an antibody-binding site of proteins A, G, L or LG, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD52. The method is used to select MAb with specificity for particular antigens. MAb can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expression vector; antibody binding protein; monoclonal antibody; Neo-R; B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Selecting monoclonal antibodies, by expressing them on the surface of hybridomas attached to antibody-binding protein, then reaction with
treating disorders characterised by inappropriate cell proliferation or cell death
                                                                                                              A haemagglutinin (HA) tag peptide (AAR81452) was expressed as a fusion with amino acids 2-221 of apoptosis-associated protein Bcl-Y (see AAR81451) following PCR amplification (see AAT17378-79) of Bcl-Y CDNA and insertion into a CWV-based pcDNA1/amp vector derivative. The HA-Bcl-Y protein was produced in vitro and in transfected COS7 and NIH3T3 cells.
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                                                                                                                                                                                                                                                                                                                                 Score 63; DB 17; Length 15; Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression vector pSEX11G2 protein G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB10433 standard; Protein; 228 AA.
                                                                       Example 1; Page 65; 100pp; English.
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                                                                                                                                                                                                                                                                                                                                      78.8%;
84.6%;
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                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         1 YPYDVPDYAGSGS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 ypydvpdyaslgs 15
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                         15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Breitling F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-1999;
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                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB10433;
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                                                                                                                                                                                                                                                                                                        The present sequence represents a haemagglutinin sequence of a chimeric adenovirus penton base protein. The peptide is encoded by overlapping oligonucleotides. The penton base protein binds to cell surface receptors called integrins. The integrins not only provide a binding site for the adenoviral penton base protein, but also mediate cellular adhesion to the extracellular matrix molecules. The specification describes a method of introducing an adenovirus into a cell in vitro having a particular molecule comprising a component that selectively binds a binding domain of the penton base protein of the adenovirus and a second component that selectively binds the cell surface binding site. A complex of the adenovirus and a second component that selectively binds the cell surface binding site. A complex of the adenovirus and the cell is montacted with it to allow entry of the adenovirus into the cell. The methods can be used for research and the vectors can be used for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                        Methods for introducing adenovirus into cells - used for genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bcl-Y; apoptosis; cell proliferation; cell death; diagnosis; gene therapy; haemagglutinin; HA tag.
                                                                            Roelvink PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kovesdi I, McVey DL,
                                                                                                                                                                                                                                                                  Example 13; Column 34; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR81452 standard; Peptide; 15 AA.
                                                                                                                                                                                                                              engineering and gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                          Bruder JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMMU-) IMMUNOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-139648/14.
                                                                                                                                      WPI; 1998-119984/11.
N-PSDB; AAV04953-54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 ypydvpdyags 24
                                 (GENV-) GENVEC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chittenden TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-1994;
09-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9605232-A1
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                                                                       Brough DE,
Wickham TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR81452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in MAD selection. This sequence represents the protein G contained in the expression vector pSEX11G2 which contains the protein G, Neo-R and the bla protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to a vaccine comprising a cell having a membrane-bound fusion protein (FP) consisting of a non-antibody immunomodulator (I) linked to a heterologous membrane attachment domain. The vaccines are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GM-CSF; granulocyte macrophage colony stimulating factor; vaccine; membrane-bound fusion protein; non-antibody immunomodulator; infection; membrane attachment domain; cancer; autoimmune disease; therapy.
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine having a membrane-bound fusion protein - comprising an Immunomodulator and heterologous membrane attachment domain useful for modulation of immune response against a disease-associated
                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                   Score 62; DB 21; Length 228;
Pred. No. 0.034;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is the pHOOK-1.GM-CSF fusion protein. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOOK-1.GM-CSF fusion protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY00874 standard; Protein; 232 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 2a-b; 91pp; English.
                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                        77.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMMU-) IMMUNE RESPONSE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US15622.
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                                                                                                                                                                                                                                                                                                               10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric - Mus sp.
Chimeric - Synthetic.
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22 ypydvpdyaga 32
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                           228 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9906544-A1
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                                                                                                                                                                           Sequence
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Sequence 51, Application US/0878933F

Patent No. 6153380

GENERAL INFORMATION:
APPLICANT: No. 615380an, Garry P
APPLICANT: Rothenberg, S. M.
TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES
FILE REFERENCE: A642601DJBRMSDS
CURRENT PELIGATION NUMBER: US/08/789,333F
CURRENT FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: 08/89,108
PRIOR APPLICATION NUMBER: 08/89,911
PRIOR PELING DATE: 1996-01-23
PRIOR PELING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
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Batent No. 6221355

GENERAL INFORMATION:
APPLICANT DOWGY

TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
ANTI-PAPHICATION NUMBER: US/09/208,966
CURRENT FILING DATE: 1998-1-10
EARLIER APPLICATION NUMBER: 60/082,402
EARLIER APPLICATION NUMBER: 60/082,402
EARLIER APPLICATION NUMBER: 60/082,402
EARLIER PILING DATE: 1998-04-20
EARLIER FILING DATE: 1997-12-10
SEQ ID NOS: 57
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 15
LENGTH: 16
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  Sednence Sed
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US-08-470-837-28
US-08-478-386A-19
US-08-452-597-19
US-08-462-498-6
US-08-922-267A-60
US-08-922-267A-60
US-08-690-011A-17
US-08-690-011A-49
US-08-685-625A-4
US-08-687-525A-4
US-08-687-525A-4
US-08-687-525A-4
US-08-887-537B-3
US-08-887-537B-3
US-08-883-898-19
US-08-883-898-19
US-08-883-733B-28
US-08-883-733B-28
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Best Local Similarity 100.
Matches 11; Conservative
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ORGANISM: human
US-09-208-966-15
      RESULT 2
US-08-789-333F-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-208-966-15
      SOFTWARE:
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Sequence 27,
Sequence 10,
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.: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
.: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
.: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
.: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
.: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-708-33F-51
US-08-700-846-10
US-08-301-071A-5
US-08-301-071A-5
US-08-990-1516-2
US-08-282-951-2
US-08-282-951-2
US-08-282-951-2
US-08-282-951-2
US-08-282-951-2
US-08-282-951-2
US-08-602-213-39
US-08-602-213-39
US-08-602-213-39
US-08-602-213-39
US-08-602-213-39
US-08-603-222-14
US-09-066-074-7
US-08-090-13988-6
US-08-91-3988-6
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Maximum DB seq
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                                                                                                                                                                                                                                                                      Sequence:
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No.
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Sequence 5, Application US/08321071A

Patent No. 5672686

CENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.
TITLE OF INVENTION: APOPTOSIS RELATED PROTEIN BC1-Y, AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004

ZIP: 20004

MEDIUM TYPE: Floppy disk
                                                                                                   Sequence 10, Application US/08700846
Patent No. 5962311
GENERAL INFORMATION:
PETRUS W.
APPLICANT: WICKHAW, THOMAS J.
APPLICANT: ROELVINK, PETRUS W.
APPLICANT: KOVESDI, IMRE
TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk.

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION UNBER: US/08/700,846

FILING DATE: 21-AUG-1996

CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 65; DB 2; Lv
Pred. No. 0.00055;
0; Mismatches 0;
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NAME: LARCHER, CAROL
REGISTRATION NUMBER: 35243
REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
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100.0%;
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TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 10: SEGUENCE CHARACTERISTICS: LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 81.2
Best Local Similarity 100.
Matches 11; Conservative
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  14 YPYDVPDYAGS 24
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STREET: TWO PRU
CITY: CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                             RESULT 4
US-08-700-846-10
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US-08-321-071A-5
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APPLICANT: Wickham, Thomas J.
APPLICANT: Kovesdi, Imre
APPLICANT: Kovesdi, Imre
APPLICANT: Kovesdi, Imre
APPLICANT: Kovesdi, Imre
TITLE OF INVENTION: THE ADENOVIRAL-MEDIATED CELL TARGETING COMMANDED BY
TITLE OF INVENTION: THE ADENOVIRAL-MEDIATED RASE PROTEIN
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                           Gaps
                                                                               FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: epitope tag
OTHER INFORMATION: sequence.
US-08-789-333F-51
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                                                                                                                                                                                                               Length 17;
                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,060
                                                                                                                                                                                                             Score 65; DB 4; Le
Pred. No. 0.00037;
0; Mismatches 0;
                                                                                                                                                                                           81.2%; SCUL.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,162
FILING DATE: 08-SEP-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: K11yk, John Jr.
REGISTRATION NUMBER: 30763
REFRENCE/CDOCKET NUMBER: 7160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 81.2
Best Local Similarity 100.
Matches 11; Conservative
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CITY: Chicago
STATE: Illinois
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APPLICANT: Wickhar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10909
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SEQ ID NO 51
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Length 25 0; Indels

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APPLICANT: YANG, ZHI
TITLE OF INVENTION: METHOD FOR ISOLATING AND DIRECTLY
TITLE OF INVENTION: DECINING GENES WHICH ENCODE CELL-SURFACE AND SECRETED
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTILSON & FOETSTET
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08990140A

| Sequence 13, Application US/08990140A
| Patent No. 6093795
| GENERAL INFORMATION:
| APPLICANT: Olsen, Henrik S. APPLICANT: Sonenberg, Nahum
| APPLICANT: Sonenberg, Nahum
| APPLICANT: Mathalie
| APPLICANT: Methot, Nathalie
| APPLICANT: Mom, Eran
| TITLE OF INVENTION: EIFGF-like Protein (PP7) Genes
| TITLE OF INVENTION: eIFGF-like Protein (P97) Genes
| FILE REFERENCE: 1488.0700001
| CURRENT APPLICATION NUMBER: US/08/990,140A
| CURRENT FILING DATE: 1996-12-13
| NUMBER OF SEQ ID NOS: 13
| SEQ ID NO 13
| LEMOTH: 10
| LEMOTH: 10
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                                                                                                                                                                        Length 219;
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Pred. No. 0.00088;
                                                                                                                                                                                                                    0; Indels
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Pred. No. 0.016;
1; Mismatches (
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STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.2%; Scc.
100.0%; Pre
0;
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Patent No. 5665590
                                                                                                                                                                     77.5%;
90.9%;
  SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.2
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                          Query Match 77.5
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                       MOLECULE TYPE: protein US-08-902-516-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                     111111111:
22 YPYDVPDYAGA 32
                                                                                                                                                                                                                                                               1 YPYDVPDYAGS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-08-282-951-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEMBRANE-BOUND CYTOKINE COMPOSITIONS
COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
RESPONSE USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 63; DB 1; Lengtn 1., Pred, No. 0.00066;
                                 CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/321,071A

FILING DATE: 11-OCT 1994

PRIOR APPLICATION S14

PRIOR APPLICATION NUMBER: US/08/321,071A

FILING DATE: 09-AUG-1995

PROR APPLICATION NUMBER: 09-8UG-1995

PROR APPLICATION NUMBER: 09-8UG-1994

ATONNEY/AGENT INPORMATION:

NAME: WIXON, HERRY N.

REGISTRATION NUMBER: 32,073

REGISTRATION NUMBER: 32,073

REGISTRATION NUMBER: 32,073

RELECOMMUNICATION INFORMATION:

TELECOMMUNICATION NUMBER: 32,073

RELECOMMUNICATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States
2 IP: 92121
COMPUTER READBLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC COMPA:DLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,516
FILING DATE: 29-JUL-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4310 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 2442
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08902516
Patent No. 5891432
GENERAL INFORMATION:
APPLICANT: SOO HOO, William
TITLE OF INVENTION: COMPRISING GM-
TITLE OF INVENTION: RESPONSE USING
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.8%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 78.8
Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YPYDVPDYAGSGS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-321-071A-5
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Gaps

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Sequence 1, Application US/08723726

Patent No. 5851521

GENERAL INFORMATION:
APPLICANT: BRANELLEC, Didier
APPLICANT: ISNER, Jeffrey M.
APPLICANT: ISNER, Jeffrey M.
APPLICANT: BENEFLE, Patrice
TITLE OF INVENTION: VIRAL VECTORS AND THEIR USE FOR TREATING
TITLE OF INVENTION: HYPERPROLIFERATIVE DISORDERS, IN PARTICULAR RESTENOSIS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                  Score 60.5; DB 1; Length 272;
Pred. No. 0.035;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 59; DB 2; Length 14;
Pred. No. 0.0026;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CITESPATITE
STATE: PA
COUNTRY: USA
ZIP: 19426-0997
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,726
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PURDR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/04493
FILING DATE: 28-MAR-1996
APPLICATION NUMBER: FR 95-04234
FILING DATE: 31-MAR-1995
ATTORREY/AGENT INNORMATION:
NAME: SAVILEY, MAITIN F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST95022A-US
TELECHMONE: (610)454-3816
TELECHMONE: (610)454-3816
                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: Mail Drop 3C43, P.O. Box 5093
CITY: Collegeville
                    75.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.8%;
83.3%;
                                                                                                                                      227 YPYDVPDYAPNKGSGT 242
                                                               12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 73.8
Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YPYDVPDYASLG 12
           Query Match
Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YPYDVPDYAGSG 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-390-874C-13
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US-08-723-726-1
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Patent No. 566590
GENERAL INFORMATION:
APPLICANT: YANG, ZHI
TITLE OF INVENTION: METHOD FOR ISOLATING AND DIRECTLY
TITLE OF INVENTION: CLONING GENES WHICH ENCODE CELL-SURFACE AND SECRETED
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 60.5; DB 1; Length 102;
Pred. No. 0.012;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33 943
REFERENCE/DOCKET NUMBER: 20296-20012.00
TELECOMMUNICATION INFORMATION:
TELEPRA: (415) 813-560
TELERA: (415) 494-0792
TELERA: 706141
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        20296-20012.00
                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,951
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/282,951 FILING DATE: 29-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                        FILING DATE: 29-UL-1994
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 30,943
REFERENCE/CDOCKET NUMBER: 2020
TELERANICATION INFORMATION:
TELEFROMMUNICATION INFORMATION:
TELEFROMMUNICATION 1415, 494-0792
TELEF. 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 272 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 75.6
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YPYDVPDYA---GSGS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-282-951-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                         linear
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APPLICATION NUMBER: US/09/265,772 FILING DATE: 10-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 73.8
Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-265-772-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YPYDVPDYAGSG 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 YPYDVPDYASLG 13
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-08-672-213-39
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                                                              APPLICANT: Williams, Lewis T.

APPLICANT: Williams, Lewis T.

TITLE OF INVENTION: A Constitutively Active
TITLE OF INVENTION: Phosphatidylinositol 3-Kinase and Uses Thereof
TITLE OF INVENTION: Phosphatidylinositol 3-Kinase and Uses Thereof
CORRESPONDENCES: 13
CORRESPONDENCES: 13
CORRESPONDENCES: 13
CORRESPONDENCES: 13
CONFORTS: Canadisco
STARET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STARET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STARET: Two Embarcadero Center, Eighth Floor
COUNTRY: USA

ZIP: 94111-3834
COMPUTER: IBN PC COMPATIBLE
SOFTWARE: PATENTION BATA:
APPLICATION NUMBER: US/08/390,874C
FILING DATE: 17-FEB-1995
CLASSIFICATION 1455
STELECOMMUNICATION INFORMATION:
REGISTRATION UNUMBER: 29,684
REFERENCE/DOCKET NUMBER: 02307K-057000US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Kiippel, Anke
TITLE OF INVENTION: A Constitutively Active
TITLE OF INVENTION: Phosphatidylinositol 3-Kinase and Uses Thereof
CORRESPONDENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
Sequence 13, Application US/08390874C Patent No. 6043062 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/09265772 Patent No. 6300111 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 16 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 73.8
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YPYDVPDYAGSG 12
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TOPOLOGY: 11
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Sequence 52, Application US/09169015
Patent No. 6180343
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Anderson, David
TITLE OF INVENTION: Green Fluorescent Protein Fusions with Random Peptides
FILE REFERENCE: A6600/DabFrmS/SJR
CURRENT APPLICATION NUMBER: US/09/169,015
CURRENT FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 55
SOGTWARE: Patentin Ver. 2.0
SEQ ID NO 52
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Pred. No. 0.0029;
0; Mismatches 2; Indels
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Patent No. 6306649

GENERAL INFORMATION:
APPLICANT: GILMAN, Michael Z.
APPLICANT: NATESAN, Sridaran
TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION
TITLE OF INVENTION: FACTORS IN GENE THERAPY
NUMBER OF SEQUENCES: 72
FILING DATE: 10 TAN 1337

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION UNMER: 08/390,874

FILING DATE: 17-FEB-1995

ATTORNEY AGENT INFORMATION:
NAME: Dow, Karen B.
RECISTRATION NUMBER: 29,684

REFERENCE/DOCKET NUMBER: 02307K-057010US

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 aming acids
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Search completed: April 11, 2002, 10:14:44 Job time: 34 sec
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Best Local Similarity 83.3'
Matches 10; Conservative
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; MOLECULE TYPE: protein
US-08-672-213-29
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Fatent No. 6306649
GENERAL INFORMATION:
APPLICANT: GILMAN, Michael Z.
APPLICANT: GILMAN, Michael Z.
APPLICANT: GILWAN, STIDATAN
TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION
TITLE OF INVENTION: FACTORS IN GENE THERAPY
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARRAD Gene Therapeutics, Inc.
STREET: 26 Landsdowne Street
CITY: Cambridge
CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59; DB 4; Length 27;
Pred. No. 0.0051;
0; Mismatches 2; Indels
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COUNTRY: USA

ZIP: 02139-4234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,213

FILING DATE: 27-JUN-1996
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,213
FILING DATE: 27-JUN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/000,553
FILING DATE: 27-JUN-1995
RILING DATE: 27-JUN-1995
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 60/019,614
FILING DATE: 29-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: BERSTEIN, DAVIG L.
REFERENCE/DOCKET NUMBER: A1,235
REFERENCE/DOCKET NUMBER: A1,235
REFERENCE/DOCKET NUMBER: A1,235
REFERENCE/DOCKET NUMBER: A1,249-0400
TELEFRAX: 617-494-0208
                    ADDRESSEE: ARIAD Gene Therapeutics, Inc. STREET: 26 Landsdowne Street CITY: Cambridge STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFRX: 617-494-0203
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
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Best Local Similarity 83.33
Matches 10; Conservative
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CORRESPONDENCE ADDRESS:
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PAPLICATION NUMBER: US 60/000,553
FILING DATE: 27-JUN-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/019,614
FILING DATE: 29-DEC-1995
ATTORNEY/AGBNI INFORMATION:
NAME: BERRYELIN, David L.
REGISTRATION NUMBER: 31,235
REFERENCE/DOCKET NUMBER: ARLAD 346B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-494-0400
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A; Residues: 1-330 < RRC>
A; Cross-references: GB:L20119
A; Experimental source: subtype H3N2
C; Superfamily: influenza virus hemagglutinin
                          HMIV15

101153

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HMIVE2

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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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39.410 Million cell updates/sec
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                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                             protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
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No.
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A; Molecule type: mRNA
A; Residues: 1-74, N/, 76-120, 'T', 122-156,'L', 158-173,'F',175-188,'S',190-200,'K',202-2
A; Cross-references: EMBL:246402; NID:9609041; PIDN:CAA86537.1; PID:9609042
A; Experimental source: isolate A/England/471/93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-74,'N',76-120,'T',122-156,'L',158-173,'F',175-188,'S',190-200,'K',202-2
A;Cross-references: EMBL:246413; NID:g609059; PIDN:CAA86548.1; PID:g609060
A;Experimental source: isolate A/Scotland/142/93
C;Superfamily: influenza virus hemagglutinin
                                                                                                                                                                                                                                                                                          A;Residues: 1134, KK,136-156, L',158-173, F',175-188, S',190-218, F',220-225, L',227
A;Cross-references: EMBL:246395; NID:9609027; PIDN:CAA86530.1; PID:91228087
A;Experimental source: isolate A/England/269/93
A;Accession: S52181
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-134, K',136-156, L',158-173, F',175-188, S',190-218, F',220-225, L',227
A;Cross-references: EMBL:246399; NID:9609035; PIDN:CAA86534.1; PID:9609036
A;Experimental source: isolate A/England/328/93
A;Accession: S52194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-134, 'K', 136-156, 'L', 158-173, 'F', 175-188, 'S', 190-218, 'F', 220-225, 'L', 227
A; Cross references: EMBL: 246414; NID: 9609061; PIDN: CAA86549.1; PID: 9609062
A; Experimental source: isolate A/Scotland/160/93
A; Accession: S52196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-134,'K',136-156,'L',158-173,'F',175-188,'S',190-218,'F',220-225,'L',227
A;Cross-references: EMBL:246415; NID:9609065; PIDN:CAA86550.1; PID:9609066
A;Experimental source: isolate A/Scotland/174/93
A;Accession: S52184
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A;Variety: isolate A/Reijing/353/89
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 20-Sep-1999
C;Accession: S52174
                                                                                                             A;MOLECULE type: mRNA
A;Residues: 1-347 <EL3>
A;Cross_references: EMBL:Z46409; NID:g609057; PIDN:CAA86544.1; PID:g609058
A;Experimental source: isolate A/Hong Kong/34/90
                         A;Cross-references: EMBL:246410; NID:9609053; PIDN:CAA86545.1; PID:9609054
A;Experimental source: isolate A/Hong Kong/23/92
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0.15;
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Pred. No. 0.15;
Mismatches
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A;Experimental source: isolate A/Beijing/353/89
C;Superfamily: influenza virus hemagglutinin
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Pred. No.
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Conservative C
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Best Local Similarity 100.
Matches 9; Conservative
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A; Residues: 1-347 <ELL>
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Best Local Similarity
Matches 9; Conserv
A; Residues: 1-347 <EL2>
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C:Species: influenza A (HIN1 and H3N2) haemagglutinin sequences obtained
A:Title: Comparison of 10 influenza A (HIN1 and H3N2) haemagglutinin sequences obtained
A:Reference number: JQ2369; MUID:94065682
A:Reference number: JQ2377
A:Reference number: GB:L20105
A:Residues: 1-331 <- Roc>
A:Residues: 1-331 <- Roc>
A:Residues: 1-331 <- Roc>
A:Residues: 1-331 <- Roc>
A:Cross references: GB:L20105
A:Cross references: GB:L20105
A:Experimental source: subtype H3N2
C:Superfamily: influenza virus hemagglutinin
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C:Species: influenza A virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: J02378
B;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A;Fitle: Comparison of 10 influenza A (HIN1 and H3N2) haemagglutinin sequences obtained A;Reference number: J02378
A;Residues: 1-331 <ROC>
A;Residues: 1-331 <ROC>
A;Residues: 1-331 <ROC>
A;Cross-references: GB:L20102
A;Experimental source: subtype H3N2
C;Superfamily: influenza virus hemagglutinin
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C; Species influenza A virus
C; Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C; Accession: S52173; S52190; S52192; S52181; S52184; S52196; S52184; S52193
R; Ellis, J.S.
Bubmitted to the EMBL Data Library, October 1994
A; Description: Antigenic and genetic variation in the haemagglutinin of recently circula A; Reference number: S52173
A; Accession: S52173
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A;Residues: 1-347 < CELL.
A;Cross-references: EMBL:246392; NID:g609020; PIDN:CAA86527.1; PID:g609021
A;Experimental_source: isolate A/Beijing/32/92
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Pred. No. 0.15;
0; Mismatches
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Pred. No. 0.15;
                                                                                                                    hemagglutinin - influenza A virus (strain SD0191)
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A; Molecule type: mRNA
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submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circ
A;Reference number: $52173
A;Accession: $52179
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R;Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circ A;Reference number: $52173
A;Accession: $52180
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hemagglutinin - influenza A virus (isolate A/England/286/93) (fragment)
hemagglutinin - influenza A virus
C:Species: influenza A Virus
A:Variety: isolate A/England/286/93
C:Date: 07-May_1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
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hemagglutinin - influenza A virus (isolate A/England/289/93) (fragment)
c;species: influenza A virus
A virus
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A virus
C;pecies: influenza A virus
C;pecies: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
A;Molecule type: mRNA
A;Residues: 1-347 <ELL>
A;Cross-references: EMBL:246396; NID:g609029; PIDN:CAA86531.1; PID:g609030
A;Experimental source: isolate A/England/284/93
C;Superfamily: influenza virus hemagglutinin
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A; Residues: 1.347 < MELL>
A; Cross-references: EMBL: 246397; NID: 9609031; PIDN: CAA86532.1; PID: 9609032
A; Experimental source: 1solate A/England/286/93
C; Superfamily: influenza virus hemagglutinin
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A;Residues: 1:347 <ELL.
A;Cross-references: EMBL:246398; NID:g609033; PIDN:CAA86533.1; PID:g609034
A;Experimental source: isolate A/England/289/93
C;Superfamily: influenza virus hemagglutinin
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R; Ellis, J.S.
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C:Species: Influenza A virus
A:Variety: Isolate A/England/247/93
A:Variety: Isolate A/England/247/93
C:Accession: 552176
R:Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circula A:Reference number: 552173
A:Reference number: 552176
A:Residues: 1-347 < ELLs
A:Residues: 1-347 < ELLs
A:Residues: 1-347 < ELLs
C:Superimental source: Isolate A/England/247/93
C:Superimental source: Isolate A/England/247/93
C:Superimental source: Influenza virus hemagglutinin
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A; Variety: isolate A/England/284/93
C; Species: influenza A virus
A; Variety: isolate A/England/284/93
C; Date: O'May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C; Accession: S52178
R; Ellis, J.S.
R; Ellis, J.S.
A; Description: Antigenic. and genetic variation in the haemagglutinin of recently circula A; Reference number: S52173
A; Accession: S52173
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R; Ellis, J.S.
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A; Description: Antigenic and genetic variation in the haemagglutinin of recently circula A; Reference number: 552173
A; Reference number: 552182
A; Molecule type: mRNA
A; Residues: 1-347 < ELLD.
A; Residues: 1-347 < ELLD.
A; Cross-references: EMBL: 246400; NID: 9609037; PIDN: CAA86535.1; PID: 9609038
A; Experimental source: 1solate A/England/346/93
C; Superfamily: influenza virus hemagglutinin
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C;Species: influenza A virus
C;Species: influence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession: S52183
C;Accession: S52183
A;Bellis, J.S.
Submitted to the EMBL Data Library, October 1994
A;Beference number: S52173
A;Reference number: S52183
A;Accession: S52183
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Riells, J.S.

submitted to the EMBL Data Library, October 1994

A) Description: Antigenic and genetic variation in the haemagglutinin of recently circula A) Reference number: 552173

A) Accession: 552185

A) Accession: 552185

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hemagglutinin - influenza A virus (isolate A/England/328/93) (fragment)
C:Species: influenza A virus
A:Variety: isolate A/England/328/93
C:Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C:Accession. 352182
Submitted to the EMBL Data Library, October 1994
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C;Species: influenza A virus
A;Variety: isolate A/England/57/94
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
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100.0%; Pred. No. 0.15;
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Best Local Similarity 100.
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submitted to the EMBL Data Library, October 1994
A; Description: Antigenic and genetic variation in the haemagglutinin of recently circ
A; Reference number: $52173
A; Accession: $52186
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REQUENCE FROM N.A.

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REDLINE=81030852; PubMed=7421990;

RA Gething M.-J., Bye J., Skehel J.J., Waterfield M.;

Gething and DNA sequence of double-stranded copies of haemagglutinin genes from H2 and DNA sequence of double-stranded copies of haemagglutinin RT denses from H2 and H3 strains elucidates antigenic shift and drift in human influenza virus.";

Lature 287:301-306(1980).

CELL RECEPTORS AND FOR INITIATING INFECTION.

CELL RECEPTORS AND FOR INITIATING INFECTION.

CHANDIAL HAMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.

CI- SUBMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.

DR PIR; A04051; HM1VH.

DR PIR; A04051; HM337; A93233.

R PIR; A04051; Hemagglutn.

DR PEAM: PPO000225; Hemagglutn.

DR PEAM: PRODOUS PROMOSES; Hemagglutn.

DR PEAM: PRODOUS PROMOSES; Hemagglutn.

CARBOHYD 24 24 N-LINKED (GLCNAC. ..) (POTENTIAL).

FT CARBOHYD 38 38 38 N-LINKED (GLCNAC. ..) (POTENTIAL).

FT CARBOHYD 97 97 N-LINKED (GLCNAC. ..) (POTENTIAL).
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21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 249;
                                                                                                                                                                                                                                                                                                                                                                                          Influenza A virus (strain X-31).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Pred. No. 0.052;
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                                                                                                April 11, 2002, 10:22:00 ; Search time 18.1 Seconds (without alignments) 28.360 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigenicity.";
J. Virol. 37:845-853(1981).
-1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: HOMOTRIMER, EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE-81194918; PubMed-6164798; Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.; Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.; Mattigenic drift in the hemagglutinin of the Hong Kong influenza subtype: correlation of amino acid changes with alterations in viral
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20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ [CONTAINS: HEMAGGLUTININ HAI CHAIN] (FRAGMENT).
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13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ [CONTAINS: HEMAGGLUTININ HAI CHAIN] (FRAGMENT).
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                                                                                                                                                                                                                                         Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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328 N-LINKED (GLCNAC. . .) (POTE
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                         328 AA.
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
                                                                        13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last seq
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                         STANDARD;
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                 J. VÎTOL. 37:845-853(1981).
-1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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Both G.W., Sleigh M.J.;
Both G.W., sleigh M.J.;
"Conservation and variation in the hemagglutinins of Hong Kong
subtype influenza viruses during antigenic drift.";
J. Virol. 39:663-672(1981).
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
                                                                          SEQUENCE FROM N.A.
MEDLINE-81194918; PubMed-6164798;
Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.;
"Antigenic drift in the hemagglutinin of the Hong Kong influenza subtype: correlation of amino acid changes with alterations in viral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 328;
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Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Envelope protein; Hemagglutinin; Glycoprotein.
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Pfam; PF00509; Hemagglutinin; 1.
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100.0%;
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NCBI_TaxID=11456
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                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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There are no restrictions on it
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-I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
                   SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
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Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D (GLCNAC. ) (POTENTIAL).
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                                                              SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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P12582; 084021; 084022;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.8%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.12; 0; Mismatches 0; Indels
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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CELL RECEPTORS AND FOR INITIATING INFECTION
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HEMAGGLUTININ HA2
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Probom; PD000225; Hemagglutinin; 1.
Probom; PD000225; Hemagglutinin; 1.
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Matches 9; Conserv
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- SUBUNIT: HOMOTRIMER, EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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BEDLINE-37265458; PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                          -LINKED (GLCNAC. . ) (POTENTIAL).
-LINKED (GLCNAC. . ) (POTENTIAL).
-LINKED (GLCNAC. . ) (POTENTIAL).
7E7ACFE716FC969A CRC64;
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P12583; Q84011;
01-0CT-1989 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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HEMAGGLUTININ HA2
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Pred. No. 0.12;
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                                                                                                                                                                PIR; A27813; HM1V//,
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; I.
ProDom; PD000225; Hemagglutni; I.
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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                                          N-LINKED (GLCNAC. .) (POTENTIAL).
K -> N (IN PIR DATA BANK).
W; A107023ACC9CC353 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-87265458; Pubmed-2440178; Kida H., Kawaoka Y., Naeve C.W., Webster R.G.; "Antigenic and genetic conservation of H3 influenza virus in wild
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P12584; Q84012; Q89793;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN; HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
                                                                                                                                                               // Match 68.8%; Score 55; DB 1; Length 550;
Local Similarity 100.0%; Pred. No. 0.12;
hes 9; Conservative 0; Mismatches 0; Indels
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Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                       HEMAGGLUTININ HA1 CHAIN.
HEMAGGLUTININ HA2 CHAIN.
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PIR; C27813; HMXV33.
InterPro; IPR001364; Hemagglutn.
Probom; PD000225; Hemagglutnin; 1.
Probom; PD000225; Hemagglutnin; 1.
Envelope protein; Hemagglutnin; 1.
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-!- FUNCTION: HEWAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPPORS AND FOR INITIATING INFECTION.

-!- SUBUNT: HOWOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.

-!- SIMILARITY: BELONGS TO THE INFUGENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-87265458; PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | HEMA_IADH4 | STANDARD; | PRT; | 550 AA. |
| 1912865; 084013; 084014; 084014; 01-0cT-1989 (Rel. 12, Last sequence update) |
| 10-0cT-1989 (Rel. 12, Last sequence update) |
| 10-0cT-1989 (Rel. 40, Last annoctation update) |
| 10-0cT-1989 (Rel. 13, Last sequence update) 
                                                                                                                                                       Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Influenza A virus (strain A/Duck/Hokkaido/7/82).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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N-LINKED (GLCNAC. . .) (F
6C30BF67CFDCB7DE CRC64;
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0.12;
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Pfam; PF00509; Hemagglutinin; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
NON_TER 1 1 1328 HEWAGGLUTININ HAL
CHAIN 330 550 HEWAGGLUTININ HAL
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                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                      Pred. No.
                                                                                                                                                       68.8%; Score 55;
100.0%; Pred. No.
Live 0; Mismatc
                                 61577 MW;
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Best Local Similarity 100.00
These 9; Conservative
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                                 550 AA;
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22
38
165
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483
550 AA;
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Best Local Similarity
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SEQUENCE FROM N.A.
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P43257;
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CHAIN
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HEMA_IADHK
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  SOUR PRINTER THE TERM TO DE REAL PROPERTY OF THE PROPERTY OF T
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-1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO ECLL RESPONSA AND FOR INITIATING INFECTION.

-1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.

-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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HEMAGGLUTININ HA2 CHAIN.
N-LINED (GLCNAC. . .) (POTENTIAL).
Y -> N (IN PIR DATA BANK).
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-87265458; Pubmed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
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                                                                                                HEMA_IADH6 STANDARD; PRT; 550 AA.
12587; 084017;
01-0CT-1899 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECIRSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
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                                                                                                                                                                                                                                                                                     Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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67BCD85F44736CFE CRC64;
                                                                                                                                                                                                                                                                  Influenza A virus (strain A/Duck/Hokkaido/9/85).
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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550 AA;
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98 YPYDVPDYA 106
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                                                            HEMA_IADH6
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HEMA_IADH7
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                                                                                                                                                                                                                                                                                                                                                                                                    VICOLOGY 159:109-119(1987).

-i- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.

-i- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.

-i- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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M-LINKED (GLCNAC...) (POTENTIAL).
M, 6EF81793281D53EB CRC64;
                                                                                                                                                                                                                                                                               MEDLINE-67265458; Pubmed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN;
HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
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Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                              Influenza A virus (strain A/Duck/Hokkaido/10/85).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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      Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
"Molecular evidence for a role of domestic ducks in the introduction of avian H3 influenca viruses to pigs in southern China, where the A/Hong Kong/68 (H3N2) strain emerged.";
J. Gen. Virol. 72:2007-2010(1991).
-!- FUNCTION: HEWAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-!- SUBJUNT: HOWOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENCA HEMAGGLUTININ FAMILY.
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                     68.8%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.12; 1.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Influenza A virus (strain A/Duck/Hong Kong/64/76).
Virusės; ssRNA negative-strand virusės; Orthomyxoviridae;
Influenza virus A and B group; Influenza A virusės;
Influenza A virus.
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ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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MEDLINE=91341491; PubMed=1875195
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Matches 9; Conservative
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Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
"Molecular evidence for a role of domestic ducks in the introduction of avian H3 influenza viruses to pigs in southern China, where the A/Hong Kong/68 (H3N2) strain emerged.";
J. Gen. Virol. 72:2007/2910.
-!- FUNCTION: HEMAGGLUTINI IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INPECTION.
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                              -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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00-NOG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN;
HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 550;
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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100.0%; Pred. No. 0.12;
ive 0; Mismatches
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HA2) LINKED BY A DISULFIDE BOND
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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Matches 9; Conserv
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-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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HEMAGGLUTININ HAZ CHAIN.
N-LINKED (GLCNAC. ..) (POTENTIAL).
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02.0AG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN;
HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                    Length 550;
                                                                                                                                                                                                                                                                                                                                                Influenza A virus (strain A/Goose/Hong Kong/10/76).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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100.0%; Pred. No. 0.12;
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
              EMBL; D00932; BAA00772.1; -.
InterPro; IPR001364; Hemagglutn.
Probon; P000025; Hemagglutnin; 1.
Probon; P000025; Hemagglutn; 1.
Envelope protein; Hemagglutnin; Glycoprotein.
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send an email to license@isb-sib.ch).
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01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1989 (Rel. 14), Last annotation update)
E0-AUG-2001 (Rel. 40), Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                     Length 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Influenza A virus (strain A/Memphis/6/86).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
N-LINKED (GLCNAC. ..) (POT.
W. 9A1E094DA28BACD2 CRC64.
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HEMAGGLUTININ HA2 CHAIN.
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                                                                                                                                                                     Score 55;
Pred. No.
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Best Local Similarity 100.
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SQ SEQUENCE 550 AA; 61804 MW; 52C9F14B309310ED CRC64;

0; Gaps Query Match

68.8%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels

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Search completed: April 11, 2002, 10:22:00 Job time: 430 sec

20         55         68.8         327         12         Q9YRUT         O9yruT         Influenza a O9yruT         O9yruT         O9yruT         Influenza a O9yruT         O9yruT         Influenza a O9yruT         O9yruT         Influenza a O9yruT         O9yruT         Influenza a O9yruT         O9yruT         O9yruT         Influenza a O9yruT         O9yruT	RESULT 1 09W821 1D 09W821 1D 09W821 1D 09W821 1D 09W821 1D 09W821 1D 01-0V-1999 (TrEMBLrel. 12, Created) 1D 01-0V-1999 (TrEMBLrel. 17, Last sequence update) 1D 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 1D 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) 1D 01-JUN-2001 (TrEMBLrel. 17, Toxyols11; 1D 01-JUN-2001 (TrEMBLrel. 17, Toxyols11; 1D 01-JUN-2001 (TrEMBLrel. 1807-1998) 1D 11 11 11 11 11 11 11 11 11 11 11 11 1	
GenCore version 4.5  Copyright (c) 1993 - 2000 Compugen Ltd.  OM protein - protein search, using sw model  Run on:  April 11, 2002, 10:22:57; Search time 50.04 Seconds  (without alignments)  40.924 Million cell updates/sec  Title:  Berfect score:  1 YPYDVPDYAGSGSK 14  Scoring table: BLOSUM62  Gapop 10.0, Gapext 0.5  Searched:  473505 seqs, 146272329 residues  Total number of hits satisfying chosen parameters:  Minimum DB seq length: 2000000000  Maximum DB seq length: 2000000000  Post-processing: Minimum Match 0%	Se : SPTREMG 2: SP_MS	No. Score Query  No. Score Match Length DB ID  1 55 68.8 236 12 09W821  2 55 68.8 236 12 09W879  4 55 68.8 236 12 09W879  5 68.8 236 12 09W879  6 55 68.8 236 12 09W124  6 55 68.8 286 12 09W125  7 55 68.8 286 12 09W124  6 55 68.8 325 12 09W124  7 55 68.8 325 12 09W124  8 55 68.8 325 12 040774  10 55 68.8 326 12 040774  11 55 68.8 327 12 092325  12 092325 influenza a 040779

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68.8%; Score 55; DB 12; Length 236; 100.0%; Pred. No. 0.25; or Indels ive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 9; Conservative
                                                               Conservative
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STRAIN-A/TAIWAN/2034/96;
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                               Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                           NCBI_TaxID=95240;
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                                                                                                                               EXEQUENCE FROM N.A.

STRAIN-TOKYO1570, TOKYO1566, TOKYO1567, TOKYO1569, TOKYO1569, Mori S., Sekine H.;

"Hal domain of Influenza A (H3N2) virus.";

Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AB013819; BAA77281.1;

EMBL; AB013809; BAA77289.1;

EMBL; AB013811; BAA77289.1;

EMBL; AB013811; BAA77289.1;

EMBL; AB013811; BAA77289.1;

InterPro; IPR01364; Hemagalutn.
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                                                                         Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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STRAIN=72, 70, AND 71;
Nagashima M., Mori S., Sekine H.;
"Influenza A virus gene for hemagglutinin.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mori S., Sekine H.;
"HAI domain of Influenza A (H3N2) virus.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB014062; BAA77294.1; -.
EMBL; AB013008; BAA77294.1; -.
EMBL; AB014060; BAA77292.1; -.
EMBL; AB014060; BAA77292.1; -.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLITININ (FRAGMENT).
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Last annotation update)
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PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
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Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
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Matches 9; Conservative
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Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
"Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in
                                                                                                                                                                                                      influenza A virus (A/Taiwan/2034/96(H3N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=95241;
                                                                                                                                                                                                                                                                                                                                                                                                                      Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
"Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             influenza A virus (A/Taiwan/2192/96(H3N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
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Pred. No. 0.31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF139937; AAD34854.1; -.
InterPro; IPR001364; Hemagglutn.
Pfam; PR00599; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF139336; AAD34853.1; -.
Interpro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 AA; 32075 MW; 7BA39C7632D33186 CRC64;
                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
H3 HEMAGGLUTININ (FRAGMENT).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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100.0%; Pred. No. v...
286 AA.
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=147149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=A/FINLAND/583/98;
Pyhala R., Haanpaa M., Kleemola M., Tervahauta R., Visakorpi R.,
Kinnunen L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.8%; Score 55; DB 12; Length 325;
llarity 100.0%; Pred. No. 0.36;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                              68.8%; Score 55; DB 12; Length 325; 100.0%; Pred. No. 0.36; Live 0; Mismatches 0; Indels
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBI_TaxID=11320;
                                                                                                                                                                  325 AA; 36103 MW; 4E5B4648C2024765 CRC64;
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325 AA; 36029 MW; 5BECB8CC3E83B1C2 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLITININ (FRAGMENT).
Influenza A virus (A/Finland/583/98(H3N2)).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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  EMBL, AFO08782; AAB63719.1: -. InterPro. IPRO01364; Hemagglutn. Pfam: PF00509; Hemagglutin; 1. ProDom; PD000225; Hemagglutn; 1.
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Vacche 0:0-0(2001).
Babb: AF111689; AA47810.1; -
InterPro; IPR001364; Hemagglutn.
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Best Local Similarity 100.
Matches 9; Conservative
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98 YPYDVPDYA 106
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STRAIN=A/TAIWAN/2191/96;
Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
"Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRnA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=95236;
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Influenza virus A and B group; Influenza A viruses.
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STRAIN-4/ILLINDIS,
STRAIN-4/ILLINDIS,
FILCH W.M., Bush R.M., Bender C.A., Cox N.J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF139932; AAD34849.1; -.
InterPro: IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutni. 1.
PRINTS; PR00329; Hemagglutni. 1.
ProDom; PD000225; Hemagglutni. 1.
NON_TER 1 1 1 1 1 NON_TER 286 SEQUENCE 286 AA; 31976 MW; 69AB2AE727D26078 CRC64;
                                                                                                              32059 MW; CB51B092AAD0D7D8 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ GENE (FRAGMENT).
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PRO0329; HEMAGGLUTN12.
PD000225; Hemagglutn; 1.
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Best Local Similarity
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286 AA;
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Osiowy C.K.;
"Generic characterization of A/Sydney/05/97-like(H3N2) Influenza virus "Generic characterization of A/Sydney/05/97-like(H3N2) Influenza virus isolates circulating in Canada during the 1997/98 Influenza season.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF087700; AAC36729.1; -.
InterPro; IPR0001364; Hemagglutin.
Probom: PF000509; Hemagglutinin; 1.
Probom: PD00255; Hemagglutinin; 1.
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STRAINA-A/SYDNEY/05/97-LIKE(H3N2);
OSIOWY C.K.;
'Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus
'Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus
isolates circulating in Canada during the 1997/98 Influenza season.";
EMBL; AF087703; AAC36732.1;
InterPro; IPR001364; Hemagglutn.
Propon;
Propon; P0000225; Hemagglutn; 1.
                                                                                                                                                                                                                            Score 55; DB 12; Length 327;
Pred. No. 0.36;
0; Mismatches 0; Indels
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Pred. No. 0.36;
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBL_TAXID=11320;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Last annotation update)
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100.0%; Pred. No. ...
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Best Local Similarity 100.
Matches 9; Conservative
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327 AA;
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Best Local Similarity
Matches 9; Conserv
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Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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STRAINA-/PENNSYLVANIA/7/94(H3NZ);
FITRAINA-/PENNSYLVANIA/7/94(H3NZ);
FITCH W.M., BUSH R.M., Bender C.A., COX N.J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF006188; AAA65725.1;
InterPro: IPR001364; Hemagglutin.
Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutinin; 1.
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NCBL_TaxID=11320;
                 Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;
Submitted (JUN'1997) to the EMBL/GenBank/DDBJ databases.
BMBL, AF008787, AAB63724.1;
InterPro; IRR001364; Hemagglutin.
Probom; P000225; Hemagglutinin; 1.
Probom; P000225; Hemagglutinin; 1.
NON_TER 1 1 1
NON_TER 326 326 A8; 36197 MW; 4B84BD4AADC44A77 CRC64;
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326 AA; 36197 MW; 4B84BD4AADC44A77 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TEMBLrel. 17, Last annotation update)
HEMAGGLUTININ GENE (FRAGMENT).
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STRAIN-A/NEW_YORK/28/94(H3N2);
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Best Local Similarity 100.
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326 AA;
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EMBL, AF087701, AAC36730.1;
InterPro: IPR001364; Hemagglutn.
Pfan; PF00509; Hemagglutin.
PRINTS; PR00329; Hemagglutin.
PRINTS; PR00329; Hemagglutin.1.
PRINTS; PR00225; Hemagglutin.1.
PRODOM; PD000225; Hemagglutin.1.
PRONO_TER 327
SEQUENCE 327 AA; 36373 MW; ADBD67D856EBCC96 CRC64;
                                                                   Oslowy C.K.;
"Genefit characterization of A/Sydney/05/97-like(H3N2) Influenza virus
"Genefit characterization of A/Sydney/05/97-like(H3N2) Influenza virus
isolates circulating in Canada during the 1997/98 Influenza season.";
Submitted (ANG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AF087709; AAC36738.1;
InterPro: IPR001364; Hemagglutin.
Probom: PD000225; Hemagglutin.; 1.
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Virusas; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus:
NCBI_TaxID-82372;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                  SEQUENCE FROM N.A. STRAIN-A/SYDNEY/05/97(H3N2);
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Haemagglutinin epi Haemagglutinin epi Haemagglutinin epi Influenza haemaglu Truncated Human p2 Truncated cyclin d Human cyclin depen Truncated Human p2

Human cyclin depen

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Haemagglutinin; epitope; monoclonal antibody; detection; isolation; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human influenza virus haemagglutinin epitope peptide fragment #3.
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AAY96075
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AAY96045
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AAB75005
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96DE-1043314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human parainfluenza virus.
WPI; 1998-241603/22
Key
Modified-site
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AAW59452
THE STATE OF A STATE O
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Peptide encoded by
Flu-epitope scramb
Flu epitope tagged
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pTAT-HA linker-enc
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Saccharomyces cere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Influenza haemaggl
                                                                                             April 11, 2002, 10:15:43; Search time 53:05 Seconds (without alignments) 18.152 Million cell updates/sec
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/ SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*

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               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                            fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                               522463 segs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
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AAW41032
AAB459116
AAB45969
AAY90725
AAY49751
AAB03963
AAG29443
AAG29463
                                                                       OM protein . protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 SGSGYPYDVPDYA 13
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Match Length
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86.7
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75 67 67 67 67 67 68 68 68 68

26432

Score

Result No.

Post-processing:

Database

Perfect score:

Run on:

Sednence:

Scoring table:

Searched:

Anti-ILB monoclona Anti-ILB monoclona

Human interleukin Human interleukin

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; 0

Indels

Length 34;

Score 71; DB 21; Pred. No. 0.00018; ); Mismatches 1;

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Conservative

Similarity

Query Match Best Local Simi Matches 12;

94.78; 92.38;

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                                                                                                This peptide fragment represents a human influenza virus haemagglutinin epitope which is used to make monoclonal antibodies with an affinity constant of 108 M·1. Such antibodies are used for detecting and isolating native human influenza virus haemagglutinin (HA), modified HA or HA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes a method for isolating one or more genetic elements encoding a gene product with a desired activity. Expression of the genetic element results, directly or indirectly in the modification of an optical property of the encoded polypeptide. The method comprises compartmentalizing the genetic elements into microcapsules, expressing them to produce their respective gene products within the microcapsules, and sorting genetic elements which produce the gene product(s) with the which encode a gene product with a desired activity. The method is used for isolating genetic elements which encode a gene product with a desired activity. This can be a catalytic, regulatory or binding activity. The present sequence represents a fusion of a flag epitope and influenza haemagglutinin. It was used in the course of the invention.
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolation of genetic elements encoding a gene product with a desired activity is carried out in microcapsules where changes in optical activity are detected -
                virus haemagglutinin - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide encoded by amplification product encoding a FLAG-HA peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetic element; optical property; gene product; microcapsule.
                                                                                                                                                                                                                                                           Length 13;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                       100.0%; Score 75; DB 19;
100.0%; Pred. No. 1.6e-05;
Live 0; Mismatches 0;
              Monoclonal antibodies to influenza virus haemagg
detecting and isolating haemagglutinin proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 12; Page 79-80; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB07730 standard; Peptide; 34 AA.
                                                                Claim 7; Page 2; 6pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JAN-2000; 2000WO-GB00030.
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                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                          1 sgsgypydvpdya 13
                                                                                                                                                                                                                                                                                                                             SGSGYPYDVPDYA 13
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N-PSDB; AAA59266.
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Best Local Similarity
                                                                                                                                                                                                        13 AA;
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                                                                                                                                                                      fusion proteins
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                                                                                                                                                                                                                                                                          Transdominant bioactive agent, phenotype alteration, signalling pathway, antitumour agent; cardiovascular disease; angiogenesis; atherosclerosis; obesity; neurodegeneration; bone disease; infection; allergy; therapy;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening for trans-dominant active agents able to alter phenotype - useful to identify potential drugs with e. g. anti-tumour activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                            AAW41032 standard; Protein; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 53; 91pp; English.
                                                                                                                                                                                                                                             Flu-epitope scrambled peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-US01048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0589911
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Best Local Similarity 91.7
Matches 11; Conservative
                             SGSGYPYDVPDYA 13
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                                                                                                                                                                                                                                                                                                                             flu-epitope peptide.
                                               Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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Intracellular transdominant bloactive agent; screening; cell phenotype; effector peptide.
                                                                                                                         Transdominant effector peptide associated screening peptide #49.
                                                                                                                                                                                                                                                                                                                                            (STRD ) UNIV LELAND STANFORD JUNIOR. (RIGE-) RIGEL PHARM INC.
                                         AAB45969 standard; Peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                      Rothenberg SM, Nolan GP;
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-060084/07.
                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                          23-JAN-1997;
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                                                                                                                                                                                                                                                 28-NOV-2000
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                                                                   AAB45969;
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                           AAB45969
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Wurine 10TJ/2 Clone 8 cells were infected with pBabe puro retrovirus constructs containing a sequence coding for the Flu scrambled epitope or an inhibitor peptide (see AAW2917) identical corpus constructs containing sequence coding for the Flu scrambled epitope or an inhibitor peptide (see AAW2917) identical to the C2 region of protein kinase C (PKA) isozymes. Control clone of colls showed predominantly cytoplasmic and perflucibles cells infected with constructs coding for the C2 region showed predominantly cytoplasmic and periluciber showed predominantly cytoplasmic and periluciber stanning in both control and PMA induced cells. Novel outcomes can staining in both control and PMA induced cells. Novel outcomes can cocur upon expression of peptides in cells. A claimed method of screening for transdominant intracellular bioactive agents (A) able to alter the phenotype of a cell comprises: (a) introducing a containing the cells for altered phenotype due to presence of (A). Also new are: (1) a library of retroviruses containing a different randomised (I); and (2) a library of ammalian cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening for transdominant intracellular active agents able to alter cell phenotype - useful for examining for changed phenotype, particularly to identify potential drugs with e. g. antitumour
                                                                                                                                                                           Transdominant intracellular effector peptide; RNA; screening; altered phenotype; retrovirus; library; signal transduction; antitumour; pBABE; influenza virus; flu; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 containing the library of (1), preferably integrated into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 67; DB 18; L. Pred. No. 0.00038; 0; Mismatches 1;
                                                                                                                                                 Flu epitope tagged scrambled peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 53; 91pp; English.
                                                                 AAW29116 standard; Peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.3%;
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96US-0589109
                                                                                                                      04-FEB-1998 (first entry)
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Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   (RIGE-) RIGEL PHARM INC
2 gggypydvpdya 13
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                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity
                                                AAW29116
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97US-0789333. 96US-0589108. 96US-0589911.

(first entry)

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                                                                                                                                                                                 This invention describes novel in vitro screening methods (1) for a transdominant intracellular bloactive agent capable of altering the phenotype of a cell. (1) comprises: (a) introducing a molecular library of randomized candidate nucleic acids into several cells; and (b) screening the cells for a cell exhibiting an altered phenotype, where the altered phenotype is due to the presence of a transdominant bloactive agent. The methods are particularly useful for screening intracellular transdominant effector peptides and RNA molecules selected inside living cells from randomized pools. (1) is also useful for introducing random libraries into cells to screen for bloactive compounds. The methods allow rapid and highly efficient screening of large numbers of random origonucleotides and their corresponding expression products in a single step. In addition, the methods allow screening in the absence of significant prior characterization of the cellular defect.
Methods for screening intracellular transdominant effector peptides and RNA molecules comprise delivering random oligonucleotides to cells, which are then screened for an altered phenotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 67; DB 22; Length 17; Pred. No. 0.00038;
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                                                                                                                                Example 1; Column 79-80; 57pp; English.
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a library (X) of fusion nucleic acids, each comprising a nucleic acid encoding a random peptide, a nucleic acid encoding a scaffold protein and a nucleic acid encoding a fusion partner (the nucleic acid encoding the random peptide is inserted internally into the scaffold protein nucleic acid). Also described are: (1) a library of fractorian vectors comprising (X); (2) a library of host cells comprising (X); and (3) a method (METHL) of screening for bioactive peptides conferring a particular phenotype, comprising providing cells containing (X). The constructs may be used in the provaling of peptide libraries. The use of the scaffold proteins (specially green fluorescent protein. (GFP)) in the fusion constructs increases cellular expression levels, increases conformational stability increases the steady state concentrations of the random peptides and increases the steady state concentrations of the random peptides and random peptide library members expressed in cells for the purposes of detecting them. The present sequence represents a peptide which comprises the influenza haemaggluttinin (HA) epitope tag embedded with comprises which is used in an example from the present invention.
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                         Fusion; scaffold protein; peptide library; green fluorescent protein; GFP; self-binding; detection; cellular expression; screening; catabolism.
                                                                                                                                                                                                                                                             Fusions of scaffold proteins with random peptide libraries for improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compact structure forming peptide; dimerisation; stability; scaffold; library screening; drug screening; gene therapy.
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Influenza haemagglutinin epitope tag containing 19mer peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.3%; Score 67; DB 21; Length 19; 91.7%; Pred. No. 0.00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compact structure forming exemplification peptide #44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                               Peelle BR;
                                                                                                                                                                                                                                                                                                 Example 2; Page 80; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY49751 standard; peptide; 38 AA.
                                                                                                                                                                                                               Bogenberger JM,
                                                                                                                                                              98US-0169015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                      (RIGE-) RIGEL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GSGYPYDVPDYA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 gggypydvpdya 13
                                                                                                                                                                                                                                    WPI; 2000-303765/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                          library screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 AA;
                                                             Influenza virus.
                                                                                      40200020574-A2
                                                                                                                                                              08-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9951625-A2
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                                                                                                                                                                                                               Anderson D,
                                                                                                              13-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY49751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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The present invention describes peptides which have a moderate or high affinity for each other, when added as extensions to both the N-terminus and C-terminus of a protein, can be used to help fold the protein into a compact structure. This compact structure is more stable to proteases. A composition (A) comprises at least a first dimerisation peptide (I) comprising the sequence (S1) that is no more than 8 amino acids long, where the composition optionally comprises a second dimerisation peptide (II): NH2-X1-X2-X3-X4-X5-COOH (S1) where X1 to X4 = Ala, Val, Ile, Leu, Trp, Phe, Met, or Try, and X5 = Lys, Arg, Asp or Glu; NH2-X1-X2-X3-X4-X5-COOH (II). The compositions of the invention are displayed intracellularly or extracellularly and are useful to identity binding proteins and molecules, and to modulate intracellular signalling pathways. A library of constrained proteins may be evaluated in vivo for its bloactive potential. The invention can be used to access molecules or tragets within living cells, and then provide for the isolation of the constrained protein which has a phenotypic effect on the living cells. The methods are also useful to identify in vitro binding partners of the constrained protein. The compositions of the invention are useful as a scaffold for gene therapy and for potential use as a therapeutic in physiological fluids. The present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel dimerization peptides which self-associate are used with other proteins to effect the formation of compact structures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Pred. No. 0.00087;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 13; 75pp; English.
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ilarity 91.7%;
Conservative (
                                                                                                                                             98US-0080444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus
                                                                        99WO-US07374
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                                                                                                                                                                                                                     (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GSGYPYDVPDYA 13
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200059935-A1
                                                                        02-APR-1999;
14-OCT-1999
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                                                                                                                                                                                                                                                                                              Anderson D;
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99US-0122757 99US-0151291

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Fusion molecules comprising protein transduction domains and therapeutic agents, useful for treating e.g. Alzheimer's and Parkinson's diseases, dementia and epilepsy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 2; 191pp; English
                 Human immunodeficiency virus
                                                                                                                                                                28-FEB-2000; 2000WO-US05097
                                                                                                                                                                                                                                                                     (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-647439/62.
N-PSDB; AAC63859.
                                                                            WO200062067-A1.
                                                                                                                                                                                                        28-FEB-1999;
29-AUG-1999;
                                                                                                                      19-0CT-2000
                                     Synthetic
                                                                                                                                                                                                                                                                                                                 SF;
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ID AAG6
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-apoptotic polypeptide which comprises a portion of an anti-apoptotic polypeptide which inhibits apoptosis of lymphocytes in combination with a transport group is described. The transport group is capable of transporting the chimaric group or fusion peptide across the cell membrane. The anti-apoptotic polypeptide is FLICE-like inhibitor protein (FLIP) which inhibits Fas and TNF mediated apoptosis by inhibiting binding of Caspase 6 to the Fas receptor complex, thus shutting off the downstream Fas signalling pathway. The chimaric group and fusion peptide are useful for inhibiting ligand-induced apoptosis by bringing them into contact with T cells. The chimaric group is useful for expanding T cells in vitro e.g. T cells specific for particular antigens such as tumour-specific antigen, for enhancing particular antigens such as tumour-specific antigen, for enhancing T cells e.g. activated CD4+ T cells in HIV infected patients. The chimaric group is also useful for therapeutic, prophylactic or classical propertides and macromolecules such as anti-apoptotic polypeptides and nucleic ancoding such polypeptides. Two primers (AAA54298) were cased to amplify the FIJP CDNA for subcloining into the Xhol-Nool slice of the pHA-TAT vector which contains the N-terminal protein transduction domain from the human immunodeficiency virus tat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein transduction domain; fusion molecule; therapeutic agent; drug targetting; drug discovery; cell transduction; bioavailability; vaccine; nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; pre-senile dementia; epilepsy; seizure; compulsive behaviour; meningitis; encephalitis; ischaemia; spongiform encephalopathy; dyslexia; age-related memory loss; Lou Gehring's disease; viral infection; HIV; bacterial infection.
                                                                                                                                                                                                                                                                                                               Fusion polypeptide useful for inhibiting ligand-induced apoptosis, comprises portion of anti-apoptotic polypeptide linked to a transport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein. Tat is a preferred transport moiety.
                                                                                                                      (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB29443 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 9; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pTAT-HA linker-encoded peptide.
                                                                                                                                                                                                          Paya C, Algeciras-schminich A;
                                                                                                                                            (PAYA/) PAYA C.
(ALGE/) ALGECIRAS-SCHMINICH A.
               05-APR-2000; 2000WO-US09002.
                                                         99US-0127867
99US-0128021
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Matches 11; Conservative
                                                                                                                                                                                                                                                 WPI; 2000-664988/64.
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2 sgypydvpdya 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 AA;
                                                                                                                                                                                                                                                                       N-PSDB; AAA54300
                                                         05-APR-1999;
06-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                             group
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The invention relates to a novel fusion molecule comprising at least one protein transduction domain (PTD) and at least one linked molecule has therapeutic or prophylatic activity against a medical condition. The invention also relates to methods of trug discovery in which the test compound is linked to a suitable transducing protein and introduced to a call, a method of killing reasonable protein and introduced to a call, a method of killing comprising a covalently linked fusion molecule; and a mammal adapted for experimental use in which at least one transduction molecule; a mammal compensation which at least one transduction molecule has been transduced into essentially all the cells of the mammal. The fusion concerniental use in which at least one transduction molecule has been transduced into essentially all the cells of the mammal. Especially a human. The linked molecule may be a vaccine, an anti-infective drug, a cardiovascular drug, an antitumour drug, an antitumour drug, an antitumour drug, an analgesic, an antitumour drug of a central or system dolecule may be a vaccine, an anti-infective drug, a cardiovascular drug, an antitumour drug for the treatment or prevention of a central or peripheral nervous system discase, Huntington's disease, and also includes pre-senile central nervous system (CNS) disorder is especially Alzheimer's age-related dementia, epilepsy and seizures, compulsive behaviour, meningitis, crapple (or related spongiform encephalopathies), dyslexia, age-related menning vioss or Lou Gehring's disease. Fusion molecules can also be used to kill virally infected cells, especially those infections. The methods are a highly effective means for transducing an also be used to trant or prevent becerving contains and used to transduce cells, especial cells, tissues, organs and seizure and used to transduce perion molecules or neutric mammal or into specific cells, tissues, organs and especial difficient transduction of the transduce of in the invention of the transduce of in the hardenian or th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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Matches 11; Conservative
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TATA-box binding protein; epitope-tagged TBP; transcription complex; TAF, TBP associated factor; TAF-interaction factor; gene expression regulator;
                                                                                                                                                                                                                                                                                                         mating factor receptor Ste2, which was used in the development of a method to prepare cells presenting on their surface a mutant G-protein coupled receptor (GPCR) binding a desired ligand which the natural receptor cannot. The method comprises generating the natural receptor cannot. The method comprises generating complete expression plasmids comprising a coding sequence for a GPCR mutated by one or more amino acids in its transmembrane and/or extracellular domains, and operatively linked expression control sequences, transforming host cells with the plasmids and contacting the cells with the ligand and isolating those which bind. GPCR are natural receptor proteins, i.e. membrane proteins that allow cells to detect molecules in the extracellular environment. Cells presenting mutant GPCR on their surfaces are useful as biosensors, with potential applications in diagnostics and environmental and
                                                                                                                                                                           Cells for surface expression of mutants of natural G-protein receptor - where the mutants can bind a ligand that the natural receptor cannot, useful as biosensors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 18; Length 481; 0.073;
                                                                                                                                                                                                                                                                                               The present sequence is the Saccharomyces cerevisiae alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62; DB Pred. No. 0.0731; Mismatches
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                                                                                                                                                                                                                                                          Example 1; Pages 13-15; 35pp; English.
                                        (BRBI-) BRITISH BIOTECH PHARM LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW73372 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.7%;
ilarity 90.9%;
Conservative
  96GB-0006126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-FEB-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FARH ) HOECHST AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 AA;
                                                                                                                                    N-PSDB; AAT85308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Influenza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        haemagglutinin.
  22-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-1998;
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                                                                               Edwards RM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a chimeric fusion protein of the invention. The specification describes a chimeric pIX protein having at least one adenoviral pIX domain and a non-native amino acid sequence. The non-native sequence is a ligand that binds to a substrate present on surface cells. The chimeric proteins are used for producing adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric pIX protein useful in an adenovirus gene transfer vector for infecting cells comprises at least one adenoviral pIX domain and a non-native amino acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha mating factor receptor; Ste2; mutant; biosensor; diagnosis; G-protein coupled receptor; GPCR; environmental monitoring; on-line process monitoring.
                                                                             Amino acid sequence of C-terminal fusion protein of pIX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.0%; Score 64.5; DB 22; Length 165; 92.9%; Pred. No. 0.0098; Live 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae alpha mating factor receptor Ste2.
                                                                                                                  pIX protein; chimeric protein; gene transfer vector
                                                                                                                                                                                                                                                                                                                                                                                                                 Wickham TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 27-28; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW27158 standard; Protein; 481 AA.
                                                                                                                                                                                                                                                                                             09-FEB-2001; 2001WO-US04233.
                                                                                                                                                                                                                                                                                                                                    09-FEB-2000; 2000US-0181163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-GB00746.
                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                             Roelvink PW, Kovesdi I,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene transfer vectors.
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N-PSDB; AAH74659.
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Matches 13; Conserv
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                                                                                                                                                                             Mastadenovirus.
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                                                                                                                                                           Synthetic.
AAG63606;
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RESULT 11 AAW27158

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This sequence represents a haemagglutinin epitope. It was used in an epitope-tagged TATA-box binding protein (TBP) that is expressed by the transgente non-human animals of the invention. The animals are used to produce TBP. TBP is used to isolate and characterise higher-order transcription complexes (from different tissue and cell types, optionally at different developmental stages). It is also used to identify new and/or specific TBP associated factors (TAFs, e.g. transcription factors, activators or inhibitors) and TAF-interaction factors, and to raise antibodies against TBP. The TAFS may be useful for regulating gene antibodies against TBP. The TAFS may be useful for regulating gene antibodies are used for affinity purification of TBP and its complexes. TBP can isolate transcription complexes from a wide variety of different tissues and cells (contrast known methods that are limited to isolation contrast complexes in the are limited to isolation contrast.
Transgenic animal expressing epitope-tagged TATA-box binding protein - for isolating higher-order transcription complexes and specific factors that associate with the protein, useful as potential
                                                                                                                                    Claim 17; Page 18; 38pp; English.
                                                                                    therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 AA;
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Query Match 81.3%; Score 61; DB 20; Length 10; Best Local Similarity 100.0%; Pred. No. 0.0019; Matches 10; Conservative 0; Mismatches 0; Indels 4 GYPYDVPDYA 13

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Ą. AAW73371 standard; peptide; 11 Haemagglutinin epitope, 1 gypydvpdya 10 12-FEB-1999 AAW73371; 13 à

TATA-box binding protein; epitope-tagged TBP; transcription complex; TAF; TBP associated factor; TAF-interaction factor; gene expression regulator; Influenza virus. haemagglutinin

EP881288-A1

02-DEC-1998

98EP-0109516. 26-MAY-1998; 97EP-0108433 (FARH ) HOECHST AG. 26-MAY-1997;

Meisterernst M, Berglund E, Kirschbaum B,

Polites G;

WPI; 1999-001394/01.

Transgenic animal expressing epitope-tagged TATA-box binding protein - for isolating higher-order transcription complexes and specific factors that associate with the protein, useful as potential therapeutic agents

Claim 17; Page 18; 38pp; English.

This sequence represents a haemagglutinin epitope. It was used in an

ö transgenic non-human animals of the invention. The animals are used to transgenic non-human animals of the invention. The animals are used to produce TBP. TBP is used to isolate and characterise higher-order transcription complexes (from different tissue and cell types, optionally at different developmental stages). It is also used to identify new and/or specific TBP associated factors (TARS, e.g. transcription factors, activators or inhibitors) and TAP-interaction factors, and to raise antibodies against TBP. The TAFS may be useful for regulating gene expression, e.g. disease-related genes, so are potential pharmaceuticals, also for identifying human analogues for use in drug screening. The antibodies are used for affinity purification of TBP and its complexes. TBP can isolate transcription complexes from a wide variety of different forms and cells contrast known methods that are limited to isolation The present invention relates to transgenic mice comprising a transgene under operational control of a myocyte-specific promoter. The transgene encodes a protein having wild-type CREB activity or dominant negative CREB activity. CREB is 43 kD basic leucine zipper transcription factor. The expression of the transgene leads to congestive heart failure (CHF). The transgenic mice are useful as genetic models of dilated cardiomyopathy or phenotypes associated with CHF. The transgenic mice are also useful for providing important basic information concerning the role of the CREB transcriptional pathway in regulating cardiac mycocyte function. These animals will also facilitate studies designed to identify Transgenic mice expressing CREB, useful as genetic models for congestive heart failure, e.g. progressive biventricular failure, cardiac dilation, decreased myocardial contractility, peripheral edema or intracardiac thrombi Gaps ö CREB; HA peptide tag; transgenic mouse; transcription factor; congestive heart failure; CHF; haemagglutinin. Score 61; DB 20; Length 11; Pred. No. 0.0021; 0; Mismatches 0; Indels 81.3%; Score ~., 100.0%; Pred. No. 0.00 ".... 0; Mismatches AAB73290 standard; Peptide; 11 AA. Disclosure; Fig 5; 19pp; English. Haemagglutinin, HA, peptide tag. from a particular cell type). 97US-0068011. 98US-0215098 29-MAY-2001 (first entry) Query Match Best Local Similarity 100. Matches 10; Conservative WPI; 2001-256289/26. (LEID/) LEIDEN J M. 4 GYPYDVPDYA 13 1:1 AA; Influenza virus US6194632-B1 18-DEC-1998; 18-DEC-1997; 27-FEB-2001 Leiden JM; AAB73290; Sequence AAB73290 RESULT g 000000000000000x à

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new drugs that can decrease the morbidity and mortality associated with the disease. The present sequence is influenza haemagglutinin (HA) peptide tag, which was used in the present invention.
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transgenic animal expressing epitope-tagged TATA-box binding protein - for isolating higher-order transcription complexes and specific factors that associate with the protein, useful as potential
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                                                                                                                            81.3%; Score 61; DB 22; Length 11; 100.0%; Pred. No. 0.0021; 1ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                    AAW73370 standard; peptide; 12 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                               Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemagglutinin epitope.
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                                                                        11 AA;
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81.3%; Score 61; DB 20; Length 12;

Query Match

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Pred. No. 0.0023;
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              100.08;
            Best Local Similarity 100. Matches 10; Conservative
                                                          4 GYPYDVPDYA 13
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Sequence 51, Application US/0878933F
Sequence 51, Application US/0878933F
Fatent No. 6153380
GENERAL INFORMATION:
APPLICANT: No. 6153380an, Garry P
APPLICANT: No. 6153380an, Garry P
APPLICANT: No. 6153380an, Garry P
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
TITLE OF INVENTION: BEFECTOR PEPTIDES AND RNA MOLECULES
CURRENT PEPLING DATE: 1996-01-23
FRIOR APPLICATION NUMBER: 08/589,108
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 17
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Sequence 52, Application US/09169015
Sequence 52, Application US/09169015
SERENAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
TITLE OF INVENTION: Green Fluorescent Protein Fusions with Random Peptides
FILE REFERENCE: A66900/DJB/RMS/SJR
CURRENT APPLICATION NUMBER: US/09/169,015
CURRENT FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
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US-08-789-333F-51
      Sequence Seq
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Pred. No. 0.00011;
0; Mismatches 1; Indels
US-08-478-386A-19
US-08-22-597-19
US-08-462-498-6
US-08-388-653-19
US-08-388-653-19
US-08-690-011A-17
US-08-690-011A-17
US-08-690-011A-17
US-08-687-559-14
US-08-700-846-19
US-08-700-846-19
US-08-87-537B-3
US-08-883-898-19
US-08-833-733B-28
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US-08-518-835-6
US-09-157-753-19
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Matches 11; Conservative
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US-09-169-015-52
          TYPE: PRT
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Sequence 15,
Sequence 4, 1
Sequence 29,
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/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
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                                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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SEQUENCE CHARACTERISTIC
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                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 20004
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APPLICANT: Leiden, Jeffery M
TITLE OF INVENTION: DOLLARD CARDIOMYOPATHY IN TRANSCENIC MICE EXPRESSING A
TITLE OF INVENTION: DOLLARD PROPERTY OF TRANSCRIPTION FACTOR IN THE
TITLE OF INVENTION: HEART
TITLE OF INVENTION: HEART
CURRENT PAPLICATION NUMBER: US/09/215,098
CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/068,011
PRIOR PILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: HA peptide tag US-09-215-098-4
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dowdy, Steven F.

TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
FILE REFERENCE: 4888/J/12-10
CURRENT APPLICATION NUMBER: US/09/208,966
CURRENT FILING DATE: 1998-104-20
EARLIER PELLING DATE: 1998-04-20
EARLIER FILING DATE: 1997-12-10
NUMBER OF SEQ ID NOS: 57
SSETWARE: PATENTIN VEF. 2.0
SEQ ID NO 15
LENGTH: 16
                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-169-015-52
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                                                                                                                                                                    Length 19;
                                                                                                                                                                                                        1; Indels
                                                                                                                                                                    Score 67; DB 4; I
Pred. No. 0.00013;
0; Mismatches 1;
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; Sequence 15, Application US/09208966
; Patent No. 6221355
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Patent No. 6194632
SEQ ID NO 52
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                    89.38;
91.78;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                        11; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 11; Conserv
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; ORGANISM: human
US-09-208-966-15
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US-09-215-098-4
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LENGTH: 11
                                                                           FEATURE:
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               Length 11;
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                                                                                                                                                                                                                                                                                                           APPLICANT: GALLO, Gregory J.
TITLE OF INVENTION: APOPTOSIS ASSOCIATED PROTEIN BBK
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-188-177-29
Sequence 29, Application US/09188177
Sequence 29, Application US/09188177
Sequence 29, Application US/09188177
Sequence 29, Application US/09188177
Sequence 20, Application US/09188177
Sequence 20, Sequence 20, Sequence 20, CORRESPONDENCE ADDRESS:
ADDRESSED: Hale and Dorr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,514C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.3%; Score 61; DB 2; Le
100.0%; Pred. No. 0.0008;
iive 0; Mismatches 0;
             Score 61; DB 4; Lo
Pred. No. 0.00062;
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104322.188
                                                                                                                                                                                                                           US-08-632-514C-29; Sequence 29, Application US/08632514C; Patent No. 5834234; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
81.3%; Scor.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: WIXON, Henry N.
REGISTRATION UNDRES: 32,073
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 29-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (202)942-8459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202)942-8484
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 14 amino acids TYPE: amino acid
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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APPLICANT: ROLLVINK, PETRUS W.
APPLICANT: ROLLVINK, PETRUS W.
TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS
TITLE OF INVENTION: USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                  Score 59, DB 1; Length 25;
Pred. No. 0.0031;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 59; DB 2; Length 25;
Pred. No. 0.0031;
0; Mismatches 2; Indels
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COMPUTRY: USA
ZIP: 60601-6780

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDIE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PATENTION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,846
FILING DATE: 21-AGG-1996
CLASSIFICATION: 51-AGG-1996
CLASSIFICATION: 51-AGG-1996
FILING DATE: ARGUER: AS23
REGISTRATION NUMBER: 35243
REGISTRATION NUMBER: 35243
REGISTRATION NUMBER: 74294
TELECOMMUNICATION NUMBER: 74294
TELECOMMUNICATION NUMBER: 74294
TELEPAX: (312) 616-5600
TELEFAX: (312) 616-5600
TELEFAX: (312) 616-5700
SEQUENCE CHARACTERISTICS:
TENEPANTION FOR SEC 1D NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900
CITY: CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 10, Application US/08700846; Patent No. 5962311; GENERAL INFORMATION:
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83.3%;
                                                                                                                                                                                                      78.7%;
83.3%;
TELEFAX: (312) 616-5700 INPORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 78.7
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                      Query Match 78.7
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-634-060-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide US-08-700-846-10
                                                                                             single
                                                                                                                                                                                                                                                                              2 GSGYPYDVPDYA 13
                                                                                                                                                                                                                                                                                                   2 GSGYPYDVPDYA 13
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                                                                          TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-08-700-846-10
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TITLE OF INVENTION: ADENOVIRAL-MEDIATED CELL TARGETING COMMANDED BY
TITLE OF INVENTION: THE ADENOVIRAL-MEDIATED CELL TARGETING
CORRESPONDENCES: 60
CORRESPONDENCES: 60
CITX: Layo Prudential Plaza, Suite 4900
STREET: Two Prudential Plaza, Suite 4900
STREET: USA
ZIP: 60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,162
FILING DATE: 08-SEP-1994
ATONNEY/AGENT INFORMATION:
NAME: K11yk, John Jr.
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71602
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/08634060 Patent No. 5712136 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-188-177-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GYPYDVPDYA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-634-060-27
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              COMPUTER EAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPOTER: IEM PC compatible
COMPOTER: IEM PC compatible
COMPOTER: TEM PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,213
FILING DATE: 27-JUN-1996
CLASSIFICATION NUMBER: US 60/000,553
FILING DATE: 27-JUN-1995
PRIOR APPLICATION NUMBER: US 60/019,614
FILING DATE: 27-JUN-1995
APPLICATION NUMBER: US 60/019,614
FILING DATE: 29-DEC-1995
APPLICATION NUMBER: 31,235
REGISTRATION NUMBER: 31,235
REGISTRATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORM: 617-494-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bonadio, Jeffrey
APPLICANT: Goldstein, Steven A.
TITLE OF INVENTION: Gene Transfer Into Bone Cells
TITLE OF INVENTION: And Tissues
WUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 59; DB 4; Le
Pred. No. 0.0052;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Parker, David
REGISTRATION NUMBER: 32,165
REGISTRATION NUMBER: UMIC:002
REFERENCE/DOCKET NUMBER: UMIC:002
TELECOMUNICATION INFORMATION:
TELEPHONE: (512) 320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08199780 Patent No. 5763416 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.7%;
90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-494-0208
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 78.7
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-672-213-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SGYPYDVPDYA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-199-780-1
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                                                                                                              APPLICANT: GILMAN, Michael Z.
APPLICANT: NATESAN, STIDARAN
TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION
TITLE OF INVENTION: FACTORS IN GENE THERAPY
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/08672213
Patent No. 6306649
GENERAL INFORMATION:
APPLICANT: GILMAN, Michael Z.
APPLICANT: GILMAN, Michael Z.
APPLICANT: USE OF HETEROLOGOUS TRANSCRIPTION
TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIAD Gene Therapeutics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,213
FILING DATE: 27-JUN-1996
CLASSIETCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,553
FILING DATE: 27-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/019,614
FILING DATE: 29-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: BERSTEIN, David L.
REGISTRATION NUMBER: 31,235
REFERENCE/CDOCKET NUMBER: 31,235
REFERENCE/COCKET NUMBER: 31,235
FILECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                   ADDRESSEE: ARIAD Gene Therapeutics, Inc. STREET: 26 Landsdowne Street CITY: Cambridge STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: ARIAD Gene Therapeutics, Inc
26 Landsdowne Street
                                                                                                                                                                                                                                                                                                                                                               ZIP: 02139-4234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/M9-DOS
                                        Sequence 39, Application US/08672213 Patent No. 6306649 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-494-0208
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 78.7
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-672-213-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                   USA
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                US-08-672-213-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-672-213-29
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STATE: Ma
COUNTRY:
                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                       METHODS AND COMPOSITIONS FOR STIMULATING BONE CELLS
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Patent No. 5952467

APPLICANT: Hunter et al., Tony
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02251
FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Parker, David L.
REGISTRATION NUMBER: 32.165
REFERENCE/DOCKET NUMBER: UMICO09P--
TELECOMUNICATION INFORMATION:
TELEPAX: (713) 789-2679
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.3%; Score 58;
83.3%; Pred. No. (
                                                                                                                                                                                             Sequence 1, Application PC/TUS9502251
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: CELLS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDORRSSEE:
ADDRESSEE: ANDORRSSEE:
ADDRESSEE: ADDRESSEE:
ADDRESSEE: ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/199,780 FILING DATE: 18-FEB-1994 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Texas
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 GCRYPYDVPDYA 417
                                    406 GCRYPYDVPDYA 417
      2 GSGYPYDVPDYA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: Ur
ZIP: 77210
                                                                                                                                                RESULT 13
PCT-US95-02251-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US95-02251-1
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US-09-066-074-7
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Pred. No. 0.095;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                     Score 58; DB 1; Length 417;
Pred. No. 0.095;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 1, Application US/08316650
; Sequence 1, Application US/08316650
; Patent No. 5942496
; General Incommentation of the particant of th
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,650
FILING DATE: 30-SEP-1994
PRIOR APPLICATION 514
PRIOR APPLICATION NUMBER: US 08/199,780
FILING DATE: 30-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: PATEK, DAVIG L.
REGISTRATION NUMBER: 32,165
REFERENCE/ODCKET NUMBER: UMIC:008
TELECOMMONICATION INMBER: UMIC:008
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.3%;
TELEFAX: (512) 474-7577
INPORMATION POR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 417 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (713) 789-2679
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 417 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (713) 789-267'
TELEX: 79-0924
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                           ; TOPOLOGY: 11near
; MOLECULE TYPE: protein
US-08-199-780-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 GCRYPYDVPDYA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GSGYPYDVPDYA 13
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Best Local Similarity
Matches 10; Conserva
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Gaps ö

Mismatches

Length 32; 1; Indels

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REFERENCE/DOCKET NUMBER: 07251/011001
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                                                    TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                        74.78;
81.88;
                                   : 619/678-5070
619/678-5099
                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: PGAL-PIN1
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                  3 SGYPYDVPDYA 13
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                     ; CLONE: P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,912A
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lise A.
REGISTRATION NUMBER: 38,347
                                                                                                                                          COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,074
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08555912A
Fatent No. 5972697
GENERAL INFORMATION:
APPLICANT: Hunter et al., Tony
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.7%; Score 56; DB 2;
81.8%; Pred. No. 0.012;
live 1; Mismatches
ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla STATE: CA
                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/555,912
FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 07251/011001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                  ZIP: 9203/
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 81.87
Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: PGAL-PINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid 'STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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92037
                                                                        USA
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                                                    STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-555-912A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-066-074-7
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C. Species: Influenza A virus (1302020 N.) Counsyle) (1707) (1159000) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1707) (1
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C;Species: influenza A virus
A;Variety: isolate A/Hong Kong/2/94
A;Variety: isolate A/Hong Kong/2/94
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession: S52191
R;Ellis, J.S.
Submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of rece
A;Reference number: S52173
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A; Residues: 1-347 <ELL>
A; Cross-references: EMBL:246408; NID:g609055; PIDN:CAA86543.1; PID:g609056
A; Experimental source: isolate A/Hong Kong/2/94
C; Superfamily: influenza virus hemagglutinin
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Pred. No. 0.17;
0; Mismatches 1; Indels
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Pred. No. 0.17;
0; Mismatches 1; Indels
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HMIV33
HMIV89
HMIV98
HMIV186
JQ1155
JQ1155
JQ1155
JQ1156
HMIVE2
HMIVE4
HMIVHA
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Matches 10; Conserv
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A; Residues: 1-347 <ELL>
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   A; Accession: S52188
       Query Match
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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75
1 SGSGYPYDVPDVA
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length: 2000000000
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A Map position: segment 4

C; Superfamily: influenza virus hemagglutinin
C; Superfamily: influenza virus hemagglutinin, homotrimer; lipoprotein; thiolester bond
C; Superds: glycoprotein, hemagglutinin, homotrimer; lipoprotein; thiolester bond
F;1-16,Domain: signal sequence #status predicted <SIG>
F;17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F;345-555/Product: hemagglutinin HA2 #status predicted <HM2>
F;355-551/Domain: transmembrane #status predicted <TM1>
F;355-551/Domain: transmembrane #status predicted <TM1>
F;18,23,37,53,68,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;254,561,564/Binding site: palmitate (Cys) (covalent) #status predicted
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R;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518
A;Title: Comparison of 10 influenza A (HINI and H3N2) haemagglutinin sequences obtain A;Reference number: JQ2369; MUID: 94065682
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C;Species: influenza A virus
C;Species: influenza A virus
C;Date: 14-Vul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: JQ2375; JQ2376
E;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A;Title: Comparison of 10 influenza A (HINI and H3N2) haemagglutinin sequences obtain
                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: genomic RNA
A;Residues: 1-565 <KAW>
A;Cross-references: GB:M24727; GB:J04336; NID:g324000; PIDN:AAA43102.1; PID:g324001
                                                         hemagglutinin precursor - influenza A virus (strain A/equine/Kentucky/2/86[H3N8]) N.Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hemagglutinin - influenza A virus (strain SN1289)
C;Species: influenza A virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
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R;Kawaoka, Y.; Bean, W.J.; Webster, R.G.
W;Irology 169, 283-292, 1989
A;Title: Evolution of the hemagglutinin of equine H3 influenza viruses. A;Reference number: A34064; MUID:89204899
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Pred. No. 0.28;
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Pred. No. 0.23
0; Mismatches
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A;Residues: 1-330 <ROC>
A;Cross-references: GB:L20115
Experimental source: subtype H3N2
C;Superfamily: influenza virus hemagglutinin
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Best Local Similarity
' has 9; Conserve
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Best Local Similarity
Matches 9; Conserv
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A;Title: Molecular evidence for a role of domestic ducks in the introduction of avian H3 A;Reference number: JQ1153; MUID:91341491
A;Reference number: JQ1153; MUID:91341491
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Molecule type: genomic RNA
A.Residues: 1-550 (KID)
A.Gross-references: GB:M19056, NID:g324208
A.Note: the sequence in GenBank entry FLAHAPA, release 106, (PID:g324209) differs from 'A.Note: the sequence in GenBank entry FLAHAPA, release 106, (PID:g324209) differs from 'A.Note: the sequence in GenBank entry FLAHAPA, release 106, (PID:g324209) differs from 'A.Map position: segment 4
C.Senetics:
A.Map position: segment 4
C.Superfamily: influenza virus hemagglutinin HA
C.Superfamily: influenza virus hemagglutinin HA
F:1320/Product: hemagglutinin HA1 #status predicted (HA1)
F:320-536/Product: hemagglutinin HA2 #status predicted (HA2)
F:320-536/Domain: transmembrane #status predicted (AM1)
F:320-536/Domain: transmembrane #status predicted (AM1)
F:320-536/Domain: transmembrane #status predicted (AM1)
F:320-536/Domain: transmembrane #status predicted (AM1) (Covalent) #status predicted F:14-466,52-277,64-76,139-473,281-305/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                         H3N2 influenza viruses from pigs in China.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hemagglutinin precursor – influenza A virus (strain A/duck/Hong Kong/7/75) (fragment) N;Confrains: hemagglutinin HA1; hemagglutinin HA2 N;Species: influenza A virus C;Species: influenza A virus C;Date: 31-Mar_1992 #sequence_revision 31-Mar-1992 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F:1-328/Product: hemagglutinin HAI #status predicted <HAI>
F:330-545/Product: hemagglutinin HA2 #status predicted <HA2>
F:8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                      - influenza A virus (strain A/swine/126/82) (fragment)
                                                                                                                                                                                                            C;Species: influenza A virus
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 18-Sep-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Pred. No. 0.27;
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Pred. No. 0.27;
0; Mismatches
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                                                                                                                                                                                                                                                                      C; Accession: A29971
R; Kida, H.; Shortridge, K.F.; Webster, R.G.
Virology 162, 160-166, 1988
A; Tille: Origin of the hemagglutinin gene of is Reference number: A94370; MUID: 88101364
A; Accession: A29971
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90.98;
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90.98;
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Matches 10; Conserva
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                                                                                                                                                                                         precursor
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Best Local Si
Matches 10
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C;Species: influenza A virus
C;Species: influenza A virus
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession: S52173; S52190; S52197; S52181; S52194; S52196; S52194; S52193
R;Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circ A;Reference number: S52173
A;Accession: S52173
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A;Residues: 1-74, N',76-120, T',122-156, L',158-173, F',175-188, S',190-200, K',202-2
A;Cross-references: EMBL:246413; NID:9609059; PIDN:CAA86548.1; PID:9609060
A;Experimental source: isolate A/Scotland/142/93
C;Superfamily: influenza virus hemagglutinin
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A;Rosidues: 1-134, K',136-156, L',158-173, F',175-188, S',190-218, F',220-225, L',227
A;Crosz-references: EMBL:246395; NID:9609027; PIDN:CAA86530.1; PID:91228087
A;Experimental source: isolate A/England/269/93
A;Accession: S52181
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A;Residues: 1-134, K',136-156, L',158-173, 'F',175-188,'S',190-218,'F',220-225,'L',227
A;Cross-references: EMBL:246399; NID:9609035; PIDN:CAA86534.1; PID:9609036
A;Experimental source: isolate A/England/328/93
A;Accession: S52194
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A; Residues: 1-134, K', 136-156, L', 158-173, F', 175-188, S', 190-218, F', 220-225, L', 227
A; Cross-references: EMBL: 246414; NID: 9609061; PIDN: CAA86549.1; PID: 9609062
A; Experimental source: 1solate A/Scotland/160/93
A; Accession: S52196
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A; Residues: 1-74, N', 76-120, T', 122-156, 'L', 158-173, 'F', 175-188, 'S', 190-200, 'K', 202-2
A; Cross-references: EMBL: 246402; NID: 9609041; PIDN: CAA86537.1; PID: 9609042
A; Experimental source: 1solate A/England/471/93
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A;Cross-references: EMBL:246415; NID:g609065; PIDN:CAA86550.1; PID:g609066
A;ExperImental source: isolate A/Scotland/174/93
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C:Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 20-Sep-1999
C:Accession: S52174
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A;Residues: 1-347 cEL3.
A;Cross=references: EMBL:246409; NID:9609057; PIDN:CAA86544.1; PID:9609058
A;Experimental_source: isolate A/Hong Kong/34/90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:246410; NID:g609053; PIDN:CAA86545.1; PID:g609054
A;Experimental source: isolate A/Hong Kong/23/92
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0.24;
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A;Reaidues: 1-347 <ELL>
A;Cross-references: EMBL:246392; NTD:9609020; F
A;Experimental source: 1solate A/Beijing/32/92
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    influenza A virus (fragment)

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A; Residues: 1-347 <EL2>
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C; Species: Influenza A virus
C; Species: Influenza A virus
C; Deters: Influenza A virus
C; Deters: Influenza A virus
C; Deters: Influenza A virus
C; Decession: J02378
R; Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A; Title: Comparison of 10 influenza A (HIN1 and H3N2) haemagglutinin sequences obtained
A; Reference number: J02369; MUID:94065682
A; Accession: J02378
A; Molecule type: mRNA
A; Residues: 1-31 < ROC>
A; Cross-references: GB:L20102
A; Experimental source: subtype H3N2
C; Superfamily: influenza virus hemaqqlutinin
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C;Species: influenza A virus
C;Accession: J02377
S;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A;Title: Comparison of 10 influenza A (HINI and H3N2) haemagglutinin sequences obtained
A;Reference number: J02369; MUID:94065682
A;Accession: J02377
A;Accession: J02377
A;Residues: 1-331 <ROC>
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                                                                                                                                                                                                                                                       Length 330;
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                                                                                                                                                                                                                                                    DB 2;
0.23;
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0.23;
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0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    · influenza A virus (strain SD0191)
                                                                                                                                                                                                                                              73.3%; Score 55; DB 100.0%; Pred. No. 0.2 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.3%; Score 55; DB 100.0%; Pred. No. 0.2 Live 0; Mismatches
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                                                  A Molecule type: mRNA
A; Residues: 1-330 < ROC>
A; Cross references: GB:L20119
Experimental source: subtype H3N2
C; Superfamily: influenza virus hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: subtype H3N2
C; Superfamily: influenza virus hemagglutinin
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1larity 100.0%; Pred. No.
Conservative 0; Mismatc
A; Reference number: JQ2369; MUID: 94065682
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Best Local Similarity 100.00
Con 9; Conservative
                                                                                                                                                                                                                                                    Query Match 73.3
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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Cyaccession: S52178
R;Ellis, J.S.
Submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circ A;Reference number: S52178
A;Accession: S52178
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C:Species: influenza A virus
A:Variety: solate A/England/286/93
C:Species: influenza A virus
A:Variety: isolate A/England/286/93
C:Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C:Accession: S52179
S:Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circ A:Reference number: S52173
A:Recently C:Reference number: S52173
                                                                                                                                                                                                             hemagglutinin – influenza A virus (isolate A/England/284/93) (fragment) C;Species: influenza A virus A A Virus A A Virus A Vir
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A;Cross-references: EMBL:Z46396; NID:g609029; PIDN:CAA86531.1; PID:g609030
A;Experimental source: isolate A/England/284/93
C;Superfamily: influenza virus hemagglutinin
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Pred. No. 0.24;
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100.0%; Pred. No. 0.24;
iive 0; Mismatches
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Conservative 0;
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Best Local Similarity
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       Query Match
Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-347 <ELL>
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C;Species: influenza A virus (isolate A/England/1/93) (fragment)

C;Species: influenza A virus

C;Date; influenza A/England/1/93

C;Date: 0'-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001

C;Accession: S52175

S;Ellis, J.S.

Submitted to the EMBL Data Library, October 1994

A;Description: Antigenic and genetic variation in the haemagglutinin of recently circula

A;Reference number: S52173

A;Accession: S52173

A;Accession: S52175

A;Molecule type: mRNA

A;Residues: 1-347 < ELLib

A;Cross-references: EMBL:246393; NID:g609024; PIDN:CAA86528.1; PID:g940547

A;Experimental source: isolate A/England/1/93

C;Superfamily: influenza virus hemagglutinin
                                submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circula A;Reference number: $52173
A;Reference number: $52174
A;Ression: $52174
A;Molecule type: mRNA
A;Residues: 1-347 < ELLD.
A;Cross-references: EMBL:246391; NID:g609022; PIDN:CAA86526.1; PID:g609023
A;Experimental source: isolate A/Beijing/353/89
C;Superfamily: influenza virus hemagglutinin
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A;Variety: isolate A/England/247/93
A;Variety: isolate A/England/247/93
A;Variety: isolate A/England/247/93
C;Species: OrMay-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession: S52176
B;Ellis, J.S.
Submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circula A;Reference number: S52173
A;Accession: S52176
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100.0%; Pre
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R;Ellis, J.S. submitted to the EMBL Data Library,
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Best Local Similarity 100.
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A; Molecule type: mRNA
A; Residues: 1-347 <ELL>
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Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Molecular evidence for a role of domestic ducks in the introduction of avian H3 influenza viruses to pigs in southern China, where the A/Hong Kong/68 (H3N2) strain emerged.";
J. Gen. Virol. 72:2007-2010(1991).
-!- FUNCTION: HERAGGLOTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-!- HOWOTHINER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISDULINE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEMAGGLUTININ HAI CHAIN.
HEMAGGLUTININ HAZ CHAIN.
N-LINKED (GLCNAC. .) (POTENTIAL).
                                      P17001
P17001
P26134
P26141
P17000
P12586
P26137
P16998
P16999
                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 40, Last nunctation update)
4EMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                      Influenza A virus (strain A/Duck/Hong Kong/7/75).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
NCBL_TaxID=11364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 550,
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HEMA_IAHRO
HEMA_IAHSA
HEMA_IAHTS
HEMA_IAHTE
HEMA_IAHUT
HEMA_IADU3
HEMA_IADA3
HEMA_IADA3
HEMA_IADA3
HEMA_IADA3
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HEMA_IABUD
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 Search time 18.1 Seconds (without alignments) 26.334 Million cell updates/sec
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P194699
P04664
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P19106
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P03435
P16995
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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HEMA_IAMAO
HEMA_IAME1
HEMA_IAME2
HEMA_IANT6
HEMA_IAUDO
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HEWA_IAHK6
HEWA_IAHK6
HEWA_IAZH1
HEWA_IAQU7
HEWA_IAQU7
HEWA_IADH7
HEWA_IADH3
HEWA_IADH3
HEWA_IADH3
HEWA_IADH4
HEWA_IADH4
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HEMA_IAME6
HEMA_IAZH2
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HEMA_IAAMI
HEMA_IAAMI
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HEMA_IAHK7
HEMA_IAHNM
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Maximum Match 100%
Listing first 45 summaries
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                                                                      OM protein - protein search, using sw model
                                                                                                 April 11, 2002, 10:22:00
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Gapop 10.0 , Gapext 0.5
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75
1 SGSGYPYDVPDYA
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                                                                                                                                                                                                                                                                                                                        VIROLOGY 162:160-166(1988).
-!- FUNCTION: HERAGGLOTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                         Kida H., Shortridge K.F., Webster R.G.; "Origin of the hemagglutinin gene of H3N2 influenza viruses from pigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
               Gaps
                                                                                                          HEWA_IAZH3 STANDARD; PRT; 550 AA.
P1134; Q84025; Q84026;
01-701-1989 (Rel. 11, Last sequence update)
20-301. (Rel. 40, Last annotation update)
HEMAGGLUTININ (CONTAINS: HEMAGGLUTININ HA1 CHAIN; HEMAGGLUTININ HA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N LINKED (GLCNAC. .) (POTENTIAL).
N; 991F6D8BCO2F24F2 (CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.7%; Score 56; DB 1; Length 550; 90.9%; Pred. No. 0.084; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                Influenza A virus (strain A/Swine/Hong Kong/126/82).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
NCBI_TaxID=11498;
             Indels
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NON_TER 1 1 1 1 CHAIN 1 328 HEMAGGLUTININ HAI CHAIN 330 550 HEMAGGLUTININ HAI
  Pred. No. 0.084;
             0; Mismatches
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HSSP: P03437; 2HMG.
InterPro; IPR001364; Hemagglutn.
Pfam; PP00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutni; 1.
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90.98;
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             10; Conservative
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96 SCYPYDVPDYA 106
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  Best Local Similarity
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Best Local Similarity
Matches 10; Conserv
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-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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SEQUENCE FROM N.A.
BEDUINE-89204899; Pubmed-2705299;
Kawaoka Y., Bean W.J., Webster R.G.;
Kawaoka Y., Bean W.J., Webster R.G.;
"Evolution of the hemagglutinin of equine H3 influenza viruses.";
Virology 169:283-292(1989).
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS '
-!- FUNCTION:
CELL RECEPTORS AND FOR INITIATING INFECTION.
CELL PROPERTORS AND FOR INITIATING INFECTION.
CELL PROPERTORS AND FOR INITIATING INFECTION.
CELL PROPERTORS AND FOR INITIATING INFECTION.

""" A DISULFIDE BOND.
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(POTENTIAL).
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                                             olfeb-1991 (Rel. 17, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
HEMAGGLUTININ HA2 CHAIN].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 565;
                                                                                                                                                                                                   Influenza A virus (strain A/Equine/Kentucky/2/86).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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InterPro; 1PR001364; Hemagglutn.
InterPro; 1PR001364; Hemagglutn.
Pfam; PF00509; HEMAGGLUTNI2.
PRINTS; PR00330; HEMAGGLUTNI2.
PRINTS; PR00331; HEMAGGLUTNI2.
PROMO331; HEMAGGLUTNI.
Propom; P0000225; Hemagglutn; 1.
Envelope protein; Hemagglutn; 1.
Envelope protein; Hemagglutnin; Glycoprotein; Signal.
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2038CC1C6C9B8BC5 CRC64;
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N-LINKED GLCNAC...)
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HEMAGGLUTININ HA2
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Pred. No. 0.086;
565 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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  STANDARD;
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                                                                                                                             Gething M.-J., Bye J., Skehel J.J., Waterfield M.;

Gething and DNA sequence of double-stranded copies of haemagglutinin genes from H2 and H3 strains elucidates antigenic shift and drift in human influenza virus."

Nature 287:301-306(1980).

-! FUNCTION: HERMGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.

-! SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.

-! SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.

PIR: A04051: HMIVH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-81194918; PubMed-6164798; Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.; Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.; "Antigenic drift in the hemagglutinin of the Hong Kong influenza subtype: correlation of amino acid changes with alterations in viral antigenicity."; J. Virol. 37:845-853(1981).
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                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. ..) (POTENTIAL).
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HEMAGGLUTININ [CONTAINS: HEMAGGLUTININ HA1 CHAIN] (FRAGMENT).
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN]
                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.3%; Score 55; DB 1; Length 249; 100.0%; Pred. No. 0.055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Influenza A virus (strain A/England/878/69).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
                                                       Orthomyxoviridae;
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                                                                                                                                                                                                                                                                                                                  Envelope protein; Hemagglutinin; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                        HEMAGGLUTININ HAI CHAIN.
                                          Influenza A virus (strain X-31).
Viruses; ssRNA negative-strand viruses; Orthomyxovi
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 AA.
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(Rel. 05, Last sequence update)
(Rel. 40, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                        MEDLINE-81030852; PubMed-7421990;
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InterPro; IPR001364; Hemagglutn.
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249 AA;
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Matches 9; Conserv
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                                                                                        NCBI_TaxID=11489
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                       FRAGMENT).
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                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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-i- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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"Antigenic drift in the hemagglutinin of the Hong Kong influenza
subtype: correlation of amino acid changes with alterations in viral
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13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ (CONTAINS: HEMAGGLUTININ HAI CHAIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB 1; Length 320; Pred. No. 0.072; O; Indels
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Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN.
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                                                                                                                                                                                                                                                                                EMBL; K03335; AAA43184.1; -.
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
Propom; P0000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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100.0%; Pred. No. v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subtype influenza viruses during antigenic drift.";
J. Virol. 39:663-65/2(1981).
-!- FUNCTION: HEMAGGLUTINI IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-!- SUBUNTT: HOMOTRAMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISCLIFIDE BOND.
-!- SIBLIARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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HEMAGGLUTININ HA2 CHAIN.
N-LINKED (GLCNAC. ..) (POTENTIAL).
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MEDLINE-82033259; PubMed-6169840;
Both G.W., Sleigh M.J.;
"Conservation and variation in the hemagglutinins of Hong Kong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMA_IABAN STANDARD; PRT; 550 AA.
P03441; Q83961; Q83962;
21-JUL-1986 (Rel. 01, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN;
                                                                                                                                                                                                                                                                                                                                      73.3%; Score 55; DB 1; Length 328; 100.0%; Pred. No. 0.072; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Influenza A virus (strain A/Bangkok/1/79).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                                                                                                                                                                                                  MW; E30A962FD6DD805B CRC64;
                                                                                                                                  HEMAGGLUTININ HA1 CHAIN.
       Envelope protein; Hemagglutinin; Glycoprotein.
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InterPro; IPR001364; Hemagglutn.
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-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INTITATING INFECTION.

-!- SUBUNIT: HOMOTRIMER. EACH POT THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HAZ) LINKED BY A DISULFIDE BOND.

-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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HEMAGGLUTININ HAZ CHAIN.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                       () (POTENTIAL).
() (POTENTIAL).
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(POTENTIAL)
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P12582; Q84021; Q84022;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-0198 (Rel. 12, Last sequence update)
01-OCT-0108 (Rel. 10, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HA1 CHAIN; HEMAGGLUTININ HA2 CHAIN)
                                                                                                                                                                                                                       Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                   FINKED (GLCNAC. . .) (Pr
FBD2EC200689CBE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Influenza A virus (strain A/Duck/Hokkaido/5/77).
                       (GLCNAC...
(GLCNAC...
(GLCNAC...
(GLCNAC...
(GLCNAC...
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InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
ProDom; P0000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
                                                                                                                                                                                                                         DB 1;
0.12;
  (GLCNAC.
                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                         Score 55; Pred. No. (
                                         N-LINKED
N-LINKED
N-LINKED
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100.0%; Pre
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550 AA;
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285
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550 AA;
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Best Local Similarity
Matches 9; Conserv
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483
550 AA;
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 RESULT 10
HEMA_IADH3
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HEMA_IADH4
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-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.

-I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISCULFIDE BOND.

-I- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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                               Gaps
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HEMAGGLUTININ HAZ CHAIN.
HEMAGGLUTININ HAZ CHAIN.
N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-STA565458, PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                        HEMA_IADH2 STANDARD; PRT; 550 AA.
1912881, 084011;
01-0CT-1999 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annoctation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAZ CHAIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 550;
  Length 550;
                                                                                                                                                                                                                                                                                       Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                               Indels
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                                                                                                                                                                                                                                                                        Influenza A virus (strain A/Duck/Hokkaido/8/80).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00509; Hemagglutin, 1.
Probom; PD000225; Hemagglutin; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
NOW, TER 1 1 1 1 CHAIN
  DB 1;
0.12;
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0.12;
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                               Mismatches
73.3%; Score 55;
100.0%; Pred. No.
ive 0; Mismatch
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                            Conservative
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Best Local Similarity
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             Local Similarity
les 9; Conserv
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                                                          YPYDVPDYA 13
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CONFLICT
SEQUENCE
 Query Match
                                                                                                                             RESULT 9
HEMA_IADH2
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                Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VITOLOGY 159:109-119(1987).
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-87265458; Pubmed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEMAGGLUTININ HAI CHAIN.
HEMAGGLUTININ HAZ CHAIN.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
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HEMA_IADH3 STANDARD; PRT; 550 AA.
P12584; Q84012; Q89793;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN;
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P12585; Q84013; Q84014;
01-002T-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN; HAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.3%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.12;
                                                                                                                                                                                                                                          Influenza A virus (strain A/Duck/Hokkaido/33/80).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutin; 1.
Prolope protein; Hemagglutinin; Glycoprotein.
NON_TER
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Matches 9; Conservative
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HEMA_IADH7
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                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                              -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                      FUNCTION: HEMAGGIUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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M-ALGREGEREDSD9DO CRC64;
                                                                                                                     SEQUENCE FROM N.A.
BEDILINE-ST265458, Pubmed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-87265458; PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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01-0CT-1989 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 550;
                       Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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                                     Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Influenza A virus (strain A/Duck/Hokkaido/9/85).
  Influenza A virus (strain A/Duck/Hokkaido/7/82).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfan; PF00509; Hemagglutinin; 1.
Probom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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Pred. No. 0.12;
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                                                                                                                                                                                                                       Virology 159:109-119(1987).
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550 AA;
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nes 9; Conserv
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                                                                               NCBI_TaxID=11360;
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                            -i- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RESPEPORS AND FOR INTIATING INFECTION.
-i- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HAZ) LINKED BY A DISULFIDE BOND.
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-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
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-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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-> N (IN PIR DATA BANK).
67BCD85F44736CFE CRC64;
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Influenza virus A and B group; Influenza A viruses;
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Pram; Pr00309; Hemagglutinin; 1.
Procom; P0000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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PIR; F27813; HMIV98.
Virology 159:109-119(1987).
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license(isb-sib.ch).
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M.; GEF81793281D53EB CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN)
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Influenza virus A and B group; Influenza A viruses;
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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Best Local Similarity 100.
Matches 9; Conservative
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InterPro; IPR001364; Hemagglutn

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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 40, Last annotation update)
HEMAGGLOTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN;
HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
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Influenza virus A and B group; Influenza A viruses;
Influenza A virus,
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Probon; PD000225; Hemagglutin; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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HEMAGGLUTININ HAZ
Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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73.3%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels

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                    74.7%; Score 56; DB 12; Length 329, 90.9%; Pred. No. 0.29;
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Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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36562 MW; 9DD1CA9187D537DF CRC64;
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FICCH W.M., Bush R.M., Bender C.A., Cox N.J.;
FICC Natl. Acad. Sci. U.S.A. 0:0-0(1997).
EMBL: AF008858; AAB69800.1; -
InterPro; IPPRO01364; Hemagglutin.
Probom; PD000225; Hemagglutin: 1.
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Q9w8j7
Q9wi26
Q9wi24
Q40774
Q9d145
Q9d145
Q90334
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09w8z1
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            4.5
Compugen Ltd
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             GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                        protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_mammal:*
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75
1 SGSGYPYDVPDYA 13
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sp_phage:*
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sp_bacteria:*
sp_fung1:*
sp_human:*
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SEAUGHANG NOR 18. No. 18. STRAIN-A/GUANDONG/25/93; MEDLINE-96105347; PubMed=7503689; MEDLINE-96105347; PubMed=7503689; MEDLINE-96105347; PubMed=7503689; MEDLINE-96105347; PubMed=7503689; MEDLINE-96105347; PubMed=7503689; Memagglutinin of recently circulating human influenza A (H3N2) viruses in the United Kingdom."; Arch. Virol. 140:1889-1904(1995). EMBL; Z46406; CAA66541.1; InterPro; IPRO01364; Hemagglutin. 1. ProDom; PD000225; Hemagglutinin; 1. ProDom; PD000225; Hemagglutinin; 1.
                                                                                                                                                                                                                                              ^{*}\mathrm{Evolution} are the racterization of recent human H3N2 influenza A isolates from Japan and China: novel changes in the receptor binding
                                                                                                                                  SEQUENCE FROM N.A.
STRALN-A/OUANDONG/28/94 (H3N2);
MEDLINE-96370797; PubMed-8774633;
Lindstrom S., Sugita S., Endo A., Ishida M., Huang P., Xi S.H.,
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
                                             Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
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SEQUENCE 344 AA; 38139 MW; C5A8CC7DBBOACBAE CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                            HAEMAGGLUTININ.
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EMBL; U48442; AAB09416.1; -
InterPro; IPR001364; Hemagglutn.
Probom; PD00509; Hemagglutinin; 1.
Probom; PD00225; Hemagglutnin; 1.
CHAIN >344
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90.98;
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      HAEMAGGLUTININ (FRAGMENT)
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Best Local Similarity 90.99
Matches 10; Conservative
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112 SCYPYDVPDYA 122
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Best Local Similarity
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                             Influenza A virus
                                                                                         NCBI_TaxID=11320;
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                                                                                                                                                                                                                            Nerome K.;
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                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-A/HONG_KONG/1/94(H3N2);
Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;
Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF008772; AABG3709.1; -
InterPro; IPR001364; Hemagglutn.
Probom; PF00509; Hemagglutnin; 1.
Probom; PF00509; Hemagglutni; 1.
NON_TER 1
NON_TER 329 AA; 36630 MW; DIDF31668818FA8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.7%; Score 56; DB 12; Length 329; 90.9%; Pred. No. 0.29; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB 12; Length 329; Pred. No. 0.29;
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Viruses; SRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
                                                                                       Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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STRAIN-A/GUANGDONG/25/93(H3N2);
STRAIN-A/GUANGDONG/25/93(H3N2);
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF008B38; AAB63765.1;
InterPro; IPR001364; Hemagglutn.
Promon: PR00509; Hemagglutnin; 1.
Probon:
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329 AA; 36566 MW; 4DD909217213F423 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HEMAGGLUTININ GENE (FRAGMENT).
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Last annotation update)
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(TrEMBLrel. 02, I
(TrEMBLrel. 17, I
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Best Local Similarity
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Matches 10; Conserve
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01-FEB-1997 (
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Gaps

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Gaps

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SEQUENCE FROM N.A.

STRAIN-TOKYO1570, TOKYO1566, TOKYO1567, TOKYO1569, MOTIA. S., SARINE H.;

MOTIA. S., SARINE H.;

MOTIA GOMBINION OF INTILUENZA A (H3N2) virus.";

Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AB013813; BAA77281.1; -..

EMBL; AB013810; BAA77288.1; -..

EMBL; AB013811; BAA77289.1; -..

EMBL; AB013811; BAA77289.1; -..

EMBL; AB013811; BAA77289.1; -..

EMBL; AB013811; BAA77289.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.3%; Score 55; DB 12; Length 236; 100.0%; Pred. No. 0.29; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-TOXY(21527, TOXY(01511;
MOTI S., Sekine H.; TOXY(01511;
MOTI S., Sekine H.; TOXY(01511;
MOTI S., Sekine H.; TOXY(1989) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB013807; BAA77285.1; --
EMBL; AB013805; BAA77284.1; --
InterPro; IPR00139; Hemagglutin.
PETAM: PF00509; Hemagglutin.
PRINTS; PR00329; Hemagglutin; 1.
PRINTS; PR00325; Hemagglutin; 1.
NON_TER
1 1
NON_TER
236 236
SEQUENCE 236 AA; 26477 MW; 4566C8E7210FB558 CRC64;
                                                                                                                                                                                                                                                    Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses. NCBL_TaxID=11320;
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Influenza virus A and B group; Influenza A viruses.
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                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGUITHIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ (FRAGMENT).
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0.29;
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                                                                            236 AA
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Pred. No.
                                                                            PRT;
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Best Local Similarity 100.
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Best Local Similarity
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NON_TER
SEQUENCE
                                                                            Q9W8Z1
Q9W8Z1;
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Q9W8T9
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                                                                                                                                                                                                                                                                                   SEUENCE FROM N.A.
STRAIN-A/HONG KONG/2/94;
STRAIN-B/HONG KONG/2/94;
STRAIN-B-56105347; PubMed-7503689;
Ellis J.S., Chakraverty P., Clewley J.P.;
Ellis J.S., Chakraverty P., Clewley J.P.;
Genetic and antigenic variation in the haemagglutinin of recently
circulating human influenza A (H3N2) viruses in the United Kingdom.";
Arch. Virol. 140:1889-1904(1995).
EMBL; 246408; CAA6653.1; ...
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutnin; 1.
Propom; P0000225; Hemagglutni; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4), COMPLETE CDS.
Influenza A virus (strain A/Equine/Kentucky/2/86).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
107-Last annotation update)
1NFLUENZA A/EQUINE/KENTUCKY/2/86 (H3N8) HEMAGGLUTININ (HA) RNA (SEG.
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Influenza virus A and B group; Influenza A viruses.
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SEQUENCE 565 AA; 63592 MW; EB9FEFF7CBB861DB CRC64;
                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HAEMAGGLUTININ (FRAGMENT).
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347 AA.
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PRT;
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Best Local Similarity 69.2
Matches 9; Conservative
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Best Local Similarity 90.9
Matches 10; Conservative
PRELIMINARY;
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109 SSNCYPYDIPDYA 121
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SEQUENCE FROM N.A.
STRAIN=A/TAINWAN/2192/96;
Shih S.-R., Chen S.-H., Wu S.-L., HO C.-C.;
Shih S.-R., Chen S.-H., Wu S.-L., Ho G.-C.;
"Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       influenza A virus (A/Taiwan/2192/96(H3N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   influenza A virus (A/Taiwan/2191/96(H3N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=95236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.3%; Score 55; DB 12; Length 286; 100.0%; Pred. No. 0.36; ive 0; Mismatches 0; Indels
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF139937; AAD34854.1; -. InterPro. IPRO01394; Hemagglutn. Ffam; PF00509; Hemagglutinin; 1. PRINTS; PR00329; HEMAGGLUTN12. NON_TER 1 1 NON_TER 286 286 SEQUENCE 286 AA; 32075 W.
                                                                                                                                                                                                                                                            Indels
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EMBL; AF139936; AAD34853.1; -.
InterPro: IPRO1364; Hemagglutn.
Pfam; PF00509; Hemagglutn., 1.
PRINTS; PR001329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
NON_TER 1 1 1
NON_TER 286 286
SEQUENCE 286 AA; 32059 MW; CB51B092AAD0D7D8 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
H3 HEMAGGLUTININ (FRAGMENT).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
H3 HEMAGGLUTININ (FRAGMENT).
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100.0%; Pred. No. 0.36;
ative 0; Mismatches 0
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Best Local Similarity
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Matches 9; Conserv
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Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
"Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=95241;
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"Hal domain of influenza A (H3NZ) virus.";
"Hal domain of influenza A (H3NZ) virus.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB01406; BAA77284.1; -.
EMBL; AB013808; BAA77286.1; -.
EMBL; AB014060; BAA77293.1; -.
EMBL; AB014060; BAA77293.1; -.
InterPro; IPR001364; Hemagglutn.
Pfam; PPG0509; Hemagglutn.
ProDom; PD000225; Hemagglutn; 1.
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Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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STRAIN-72, 70, AND 71;
STRAIN-72, 70, AND 71;
STRAIN-72, 70, AND 71;
STRAINE M., MOYI S., Sekine H.;
"Influenza A virus gene for hemagglutinin.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-UNW-2001 (TrEMBLrel. 17,
H3 HEMAGGLUTININ (FRAGMENT).
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Best Local Similarity
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SEQUENCE
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SEQUENCE FROM N.A.
STRAIN-A/TALWAN/2191/96;
Shin S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
Shin S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
Shin S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in Talwan.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF139332; AAD34849.1;
EMBL: AF139332; Hemagglutin.
Pfam: PF00509; Hemagglutinin: 1.
Prodom: PR00329; Hemagglutinin: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                              73.3%; Score 55; DB 12; Length 286; 100.0%; Pred. No. 0.36; 1.ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBI_TaxID=11320;
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SETAIN-A/ILLINOIS/5/95(H3NZ);
Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, *RF008782; AAB63719.1;
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutn.i. 1.
Probom: PD000225; Hemagglutn; 1.
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                                                                                                                                                                                                                                                                                                                                                      286 AA; 31976 MW; 69ABZAE727D26078 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    040774;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ GENE (FRAGMENT).
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 AA.
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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Q9DL45;
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A Thundan M., Kleemola M., Tervahauta R., Visakorpi R., Pyhala R., Haanpaa M., Kleemola M., Tervahauta R., Visakorpi R., A Kinnunen L.;

"Acceptable protective efficacy of influenza vaccination in young military conscripts in circumstances of incomplete antigenic and genetic match.";

"Vaccine 0:0-0(2001).

"Vaccine 0:0-0(2001).

"InterPro; IPR001364; Hemagglutn.

"PRINTS; PR00329; Hemagglutn.

"PRINTS; PR00329; Hemagglutn.

"PRINTS; PR00325; Hemagglutn.

"PRINTS: PRO00225; Hemagglutn.).
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325 AA; 36029 MW; 5BECB8CC3E83B1C2 CRC64;
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Matches 9; Conservative
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